

Report version 5.1.6
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on nucleotide - nucleotide search, using sw model

Run on: June 15, 2003 24:10:18 - Search time 206.63 seconds
(without alignment)
9822.000 Million cells of probes

US-08-826-361a-2

Perfect score: 1251
Sequence: 1 ATGATATTAAGGATTCACAG.....ACCTAGGAGATGAGAGATCA 1251

Scoring table: IDENTITY_MNF
Gapop 10.0, Gapext 1.0

Searched: Z1AS234 seqs 112644194 residues

Total number of hits satisfying chosen parameters: 4770179

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 120 summaries

Database:

1: N_geneseq_101002.*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB	ID	Description
1	1251	100.0	1251	18	AA188413	Human oestrogen re
2	1251	100.0	1251	24	AA172153	cgna encoding pr
3	1249	99.8	1257	18	AA188414	Human oestrogen re
4	1249	99.8	1257	24	AA172154	cgna encoding pr
5	1247	99.7	1434	18	AA188412	Human oestrogen re
6	1247	99.7	1434	24	AA172129	cgna encoding pr
7	1247	99.7	1460	18	AA162943	Human oestrogen re
8	1247	99.7	1647	20	AA162949	Human oestrogen re
9	1247	99.7	1646	20	AA162944	Human oestrogen re

10	1247	99.7	1740	22	AA159897	Human oestrogen re
11	1247	99.7	1808	24	AA172144	Full length oest
12	1247	99.7	1936	18	AA188415	Human oestrogen re
13	1247	99.7	2011	22	AA188412	Human oestrogen re
14	1247	99.7	2011	22	AA188415	Human oestrogen re
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91	1247	99.7	2443	24	AA188415	Human oestrogen re
92	1247	99.7	2443	24	AA188415	Human oestrogen re


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UY 721 ATGATGATGTCCTGACGAAATTTGAGGAGAAAGCTGCTGACGAAATGCTGAGGCTG 784
DB 721 ATGATGATGTCCTGACGAAATTTGAGGAGAAAGCTGCTGACGAAATGCTGAGGCTG 780
UY 781 AAGAGAGATTCAGGCTTTCTGAGGCTTCAAGCTGCTGAGGCTTCAAGGCTTCAAGGCT 840
DB 781 AAGAGAGATTCAGGCTTTCTGAGGCTTCAAGCTGCTGAGGCTTCAAGGCTTCAAGGCT 840
UY 841 TTTTGTATGAGCTATTAATATATGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 900
DB 841 TTTTGTATGAGCTATTAATATATGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 900
UY 901 GTCATCTTCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 960
DB 901 GTCATCTTCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 960
UY 961 CTTGAGGAGATTTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1020
DB 961 CTTGAGGAGATTTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1020
UY 1021 GATGAGGAGATTTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1080
DB 1021 GATGAGGAGATTTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1080
UY 1081 GTCATCTTCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 1140
DB 1081 GTCATCTTCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 1140
UY 1141 AATGAGGAGATTTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1200
DB 1141 AATGAGGAGATTTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1200
UY 1201 GAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1249
DB 1201 GAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1249

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RESULT 4
AA172146
ID AA172146 standard, cDNA, 1257 BP.
XX
AC AA172146:
DT 25-MAR-2002 (first entry)
XX
DE cDNA encoding ER splice variant ER-alpha.
XX
KW DNA binding domain; DBD; ligand binding domain; LBD; chimeric receptor;
KW estrogen receptor; ER; chromosome 14; ER-alpha; ER-beta; exon 6; ERK;
KW postreceptor; postreceptor; receptor; amplification; p107;
KW polymerase chain reaction; PCR; region; splice variant; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT 1..1257
FT /ftat a
FT /product "ER-alpha"
XX
FN ER16264 A2.
XX
PD 12-DEC-2001.
XX
PE 25-MAR-1997; 2003EP-0202021.
XX
PR 25-MAR-1994; 96EP-0200829.
PR 22-NOV-1996; 96EP-0204284.
PR 25-MAR-1997; 97EP-0200903.
XX
PA (ALU) AK20 NOBEL NV.
XX
PI Moselman S, Dijkema K.

```

PS MIT: 2002-06441472.  
DB P-PSDB: AA047856.  
XX  
PT New isolated chimeric receptor comprising a DNA binding domain and/or  
PT ligand binding domain of a new estrogen receptor, for identifying  
XX functional ligands or hormonal analogs for the receptor  
XX  
PS Example B: Page 23: 35pp: English.  
XX  
XX The sequences given in AA172146 and AA172153 encode splice variants  
XX of a novel estrogen receptor (ER). The gene encoding this new ER is  
XX located on chromosome 14 and has a different tissue distribution from  
XX classical ER. This ER also has two orphan ERs, ER-alpha and ER-beta.  
XX These orphan receptors have estrogen receptor related structure but do  
XX not appear to be able to bind estradiol or other ER ligands. These  
XX splice variants differ from the parent ER around exon 8. One clone  
XX contains exon 8b through alternative splicing. This causes an immediate  
XX termination of the reading thereby creating a truncation at the carboxy  
XX terminus. The other splice variant contains an alternative exon 8, exon  
XX 8c, which encodes two C-terminal amino acids and then has a stop codon.  
XX The splice variant proteins do not contain the AF-2 region and therefore  
XX probably lack the ability to modulate transcription of target genes in  
XX a ligand dependant manner. However they may be able to interfere with  
XX the functioning of the WT classical ER or the novel ER of the invention,  
XX either by heterodimerisation or by occupying estrogen response elements  
XX or by interactions with other transcription factors.  
XX  
XX Sequence 1257 BP: 297 A; 327 C; 455 G; 278 T; 0 other;  
XX  
XX Query Match 99.8%; Score 1249; DB 24; Length 1257;  
XX Post local similarity 100.0%; Pred. No. 0;  
XX Matches 1249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
UY 1 ATGCAATTACAGCATTCCTAGCAATCTCACTAATCTGAGGCTGAGCTGAGTACAC 60  
DB 1 ATGCAATTACAGCATTCCTAGCAATCTCACTAATCTGAGGCTGAGCTGAGTACAC 60  
UY 61 ACAGGCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120  
DB 61 ACAGGCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120  
UY 61 AATGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120  
DB 61 AATGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120  
UY 121 CACTATTCATCTGATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 180  
DB 121 CACTATTCATCTGATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 180  
UY 121 CACTATTCATCTGATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 180  
DB 121 CACTATTCATCTGATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 180  
UY 181 GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 240  
DB 181 GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 240  
UY 241 GAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 300  
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DB 461 AAGAGAGATTCAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 420  
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DB 421 GATGAGGAGATTCAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 480  
UY 481 ATGCTGAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 540  
DB 481 ATGCTGAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 540  
UY 481 ATGCTGAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 540  
DB 481 ATGCTGAGGCTGAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 540  
UY 541 AGTGGTACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 600  
DB 541 AGTGGTACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 600

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781 AATGAATATTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 840
 994 AATGAATATTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1053
 841 TGTGGATATGAGATTTTAAATGATGAGACATCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 900
 1054 TGTGGATATGAGATTTTAAATGATGAGACATCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1113
 901 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 960
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 1021 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1080
 1244 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1293
 1081 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1140
 1294 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1353
 1141 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1200
 1354 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1413
 1201 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1247
 1414 CTGATCTTCAGATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 1460

RESULT 9

AAX24 64
 10 AAX24 864 standard: cDNA: 1686 bp.

AAX24 644:

07 JUN 1999 (first entry)
 Human oestrogen receptor beta cDNA.
 oestrogen receptor beta; HER beta; human; ss.

Homo sapiens
 Key location/Qualifiers
 94..1686
 /tag 4

W0907847.A1

18 FEB 1999.

20 JUL 1998: 9860-081494.

05 AUG 1997: 9708-0906465.

(AMMP) AMERICAN HOME PROD CORP.

Bhat RA, Hedgeson RA, Hsiao C, Karabanasis SK

W01: 1999 167424/14.

P-PSDB: AAW97858.

Human oestrogen receptor beta coding sequence - useful in the

production of human oestrogen receptor-beta and identification of

human oestrogen receptor beta interactive compounds

claim 1: Page 41 42: 49pp; English.

(HER-beta, see AAW97858) containing 45 previously unknown N-terminal
 amino acid residues that are believed to contribute to the
 transcription activation function of the receptor. Human testis
 cDNA was subjected to PCR using primers (see AAX24 665-66) designed to
 supplement the previously known partial human sequence with 2
 missing N-terminal residues (Met and Thr) found in rat ER-beta,
 and to supply an artificial Kozak translation initiation sequence.
 A fragment of approximately 1500 bp was obtained, and was cloned
 into vector pCMNA3 for sequencing. The 5' sequence was confirmed
 by PCR amplification from a human ovary cDNA library and by 5'RACE
 (see AAX24 667-71). HER-beta is selectively expressed in the thymus,
 spleen, ovary and testes. The invention encompasses HER-beta
 polypeptides and polypeptides, particularly peptides which
 include residues 1-45 of HER-beta. The invention also provides
 expression systems in which transcriptionally active HER-beta or
 fragments can be produced, as well as screening methods for
 identifying HER-beta agonists and antagonists (including
 tissue specific oestrogens and anti oestrogens) and HER-beta
 co-activators and inhibitors.

Sequence 1686 bp: 413 A; 449 C; 441 G; 384 T; 0 other.

Query Match 99.78; Score 1247; DB 20; Length 1686;

Best Local Similarity 100.08; Prod. No. 0;

Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGATATATGACATCTTCAGCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 60

254 ATGATATATGACATCTTCAGCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 412

61 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 120

413 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 372

121 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 180

473 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 442

181 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 240

443 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 492

241 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 300

493 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 552

801 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 460

553 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 612

461 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 420

613 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 672

421 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 480

673 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 532

481 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 540

743 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 792

541 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 600

793 AATGATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 852

601 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 660

853 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 912

661 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 720

913 CAGTATATCTTCTGAGACATCAATCTTCAGCAATCTGAGCCTCTTGAGACATC 972


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UY 721 ATCATGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGACACAGCGGCGG 780
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DB 978 ATATGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1037
    |||||||
UY 781 AATCAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 840
    |||||||
DB 1038 AATCAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1097
    |||||||
UY 841 TGTGTGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 900
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DB 1098 TGTGTGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 1157
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UY 901 CTCATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 960
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DB 1158 CTCATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 1217
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DB 1218 GTGGCAATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1277
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UY 1021 CATCAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1080
    |||||||
DB 1278 CATCAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1337
    |||||||
UY 1081 GTCAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1140
    |||||||
DB 1338 GTCAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 1397
    |||||||
UY 1341 AGCGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 1400
    |||||||
DB 1498 AGCGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 1457
    |||||||
UY 1491 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 1547
    |||||||
DB 1498 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 1504
    |||||||

RESULT 11
AA172144
ID AA172144 standard; cDNA: 1898 bp.
XX
AC AA172144:
XX
DB 25 MAR-2002 (first entry)
XX
DB Full length estrogen receptor cDNA.
XX
DB DNA binding domain; DBD; ligand binding domain; LBD; chimeric receptor;
XX
DB estrogen receptor; ER; chromosome 14; ER alpha; ER beta; exon 8;
XX
DB estradiol; nuclear receptor; progesterone receptor; SR.
XX
DB Homo sapiens.
XX
DB Key Location/Qualifiers
XX
DB CDS 77..1669
XX
DB /tag a
XX
DB /product "Full length ER"
XX
DB EPI162264 A2.
XX
DB 12 DEC 2001.
XX
DB 25 MAR 1997; 2901BP-0202921.
XX
DB 26 MAR 1996; 96BP-0200820.
XX
DB 22 NOV 1996; 96BP-0203284.
XX
DB 25 MAR 1997; 97BP-0200903.
XX
DB (AKR) AKZO NOBEL NV.
XX
DB Mosselman S, Dijkema R.
XX

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DB WP1: 2502-084414/2.
DB P-PSDB: AAB47835.
XX
DB New isolated chimeric receptor comprising a DNA binding domain and/or
DB ligand binding domain of a new estrogen receptor. For identifying
DB functional ligands or hormonal analogs for the receptor
XX
DB Example A; Page 26; 48pp; English.
XX
DB This sequence encodes a full length novel estrogen receptor (ER). The
DB additional 5' and 3' sequences of this sequence, compared to the ER
DB sequence given in AA172148, were generated using RAE perk. The gene
DB encoding this new ER is located on chromosome 14 and has a different
DB tissue distribution from classical ER. This ER also has two orphan ER's,
DB ER-alpha and ER-beta. These orphan receptors have estrogen receptor
DB related structure but do not appear to be able to bind estradiol or other
DB ER ligands. The DNA binding domain (DBD) and ligand binding domain (LBD)
DB from this ER may be used in the chimeric receptor of the invention
DB which also has an N-terminal domain. The chimeric receptor, or DNA
DB encoding it, is useful in a screening assay for identification of new
DB drugs. Similar chimeric receptors comprising the LBD of the new ER,
DB and also comprising the DBD and an N-terminal domain derived from
DB another nuclear receptor (e.g., progesterone receptor, are useful for the
DB screening of compounds to identify new ligands or hormone analogs which
DB are able to activate the new ER. Chimeric receptors comprising a DBD
DB of the new ER, and LBD and an N-terminal domain derived from
DB another nuclear receptor, can be used to identify new ligands or
DB hormone analogs for the nuclear receptors.
XX
DB Sequence: 1898 bp; 452 A; 506 C; 501 G; 439 T; 0 other;
DB
DB Query Match 99.78; Score 1247; DB 24; Length 1898;
DB Best Local Similarity 100.08; Pred. No. 0;
DB Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB
DB 1 ATGATTTACAGCATTTGCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGAT 60
DB 246 ATGATTTACAGCATTTGCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGAT 295
DB 416 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 475
DB 496 ACAGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 455
DB 121 CAGTTATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 180
DB 456 CAGTTATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 415
DB 181 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 240
DB 416 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 475
DB 241 GTCAGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 400
DB 476 GTCAGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 535
DB 401 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 460
DB 546 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 595
DB 401 AAAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 420
DB 596 AAAAGATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGAT 655
DB 421 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 480
DB 656 GATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 715
DB 481 ATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 540
DB 716 ATGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 775
DB 541 AGTCCTGCAAACTGGCGGCAAGACAGTGGTACACATGATGATGATGATGATGAT 600
DB |||||||

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271 AGGATCTGACTCTTGGGCTCTCTGAGGCAATTCAGGCAATTCATGATGAGATTT 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 AAGAGCAATTCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 431 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 341 ATTCTGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 721 ATCTGCTGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 TGGCAATTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 781 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 841 GGTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 AAGG-----CTAAGCAATTCGCAATTAATTAATTAATTAATTAATTAATTA 608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 901 AAGCAATTCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 609 GGTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 651
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 961 AGTCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 652 AGCTCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1021 CTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1080
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 706 TTTAAATAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1081 TTTAAATAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 766 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 825
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1141 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 826 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1201 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 886 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 945
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1261 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 946 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1005
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1321 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1006 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1065
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1481 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1066 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1441 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1123 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1501 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1183 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1561 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1243 GGTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 1300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 27
AAA92174
ID AAA92174 standard; UNK: 1728 bp.
XX
AC AAA92174:
XX
DB 05-JAN-2001 (first entry)
XX
DE Oryzias latipes oestrogen receptor encoding RNA seq. ID N172.
XX
XX Oryzias latipes: oestrogen receptor; ds.
XX
OS Oryzias latipes.
XX
FN J02000.201688-A.
XX
PE 25-JUL-2000.
XX
PE 05-APR-1999: 99JP-0098787.
XX
PE 10-NOV-1998: 98JP-0319465.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
DE WPI: 2009-567960/53.
XX
DE P-PDB8: AAB20897.
XX
PI An estrogen receptor gene and its application
XX
Claim 3: Page 11-13; 23pp; Japanese.
XX
CC The present sequence encodes an estrogen receptor derived from
CC Oryzias latipes. Also described are: (1) a vector comprising the
CC oestrogen receptor gene; (2) a transformant prepared by introducing
CC the oestrogen receptor gene of vector from (1) into a host cell;
CC (3) a method for the preparation of an estrogen receptor comprising
CC culturing the transformant from (2) to produce the estrogen receptor;
CC and (4) a method for the evaluation of estrogen receptor activating
CC ability of a chemical substance in which the chemical substance is
CC reacted with a transformant prepared by introducing a reporter gene
CC connected downstream of a transcription controlling region containing
CC an estrogen non-inducible host cell. The transformant can be used for
CC the evaluation of estrogen receptor-activating ability of a chemical
CC substance.
XX
SD Sequence 1728 bp: 378 A; 514 C; 497 G; 349 T; 0 other.
XX
Query Match: 25.5%; Score 332.4; DB 21; Length 1728;
Host Local Similarity 61.4%; Pred. No. 20-77;
Matches 628; Conservative 0; Mismatches 346; Indels 48; Gaps 4;
QY 274 GATGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 409 GATGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 434 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 469 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 494 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 529 TGGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 588
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 454 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 589 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 495 -----CTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 649 GGTGCTGCTGGAAGATCTTGAAGGCTTTTAAATAGATCTGAGGCAATTCATGATTA 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


D6	124	ATGAGTGGGACAAATTCTTTAAAGATTAAGCGTCAGAGAACATGGGAGAGGGAAGAGGTGAAA	1402
OY	559	GACTTGCCGCGGAAAGCAAGAAGATGGAGGAGAGCAGCGGCAGATGCC-----	607
D6	1403	GTCAGCTCTGCGTGGAGAACAGCATGCAAGCCTTTTCCGCAAGGCAAGGCGCTATATGATAA	1462
OY	608	-----GGAGAGCTGCTCTTCTGGAGAGCGCGTGAAGAGGATAGAGTGTGACAGCTG	657
D6	1463	CAGTTTAAAGAAAGAAATGATGAGCTCTTGCTCTTGAAGAGTGAAGATGAGTATGAGCTTG	1422
OY	658	CTTAGAGCTGAAGCGGCTATATGAGTAAGG-----AGCGGCGCAAGTGGCTTGTACAAAG	714
D6	1423	TTCAGAGCTGAGAGCGCGCAATATCTATCTGAGATATATATCTGATAGAGCGCTGACATAA	1482
OY	715	GGCTTCATGACATATCTGCTGCAACAATGAGAGAGAGAGAGAGAGCTGGCTGACAGATGAGAG	774
D6	1483	CTTTGATATATAGAGCTTATCTGAGCAAGCTGAGAGAGAGAGAGAGTGGTGTGACATGATCAA	1542
OY	775	TGGAGCAAGACATATCTGAGCTTGTGTCAGAGTCAAGCTTGTTCAGCAAGCGATAGAGCTGG	834
D6	1543	TGGAGCAAG	1602
OY	835	GATGAGTGTGTGATGAGAGATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	894
D6	1603	GAAAGCGCTGCGGTAGACATATCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1662
OY	895	GATGAGTGTGTGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	954
D6	1663	GTCAGAGATGAG	1722
OY	955	GATGAGTGTGTGATGAG	1014
D6	1723	GATGAGTGTGTGATGAG	1782
OY	1015	CTGATGAG	1074
D6	1783	CTGATGAG	1842
OY	1075	CTGATGAG	1134
D6	1843	ATATGAG	1902
OY	1132	AATGAG	1191
D6	1903	GATGAG	1962
OY	1192	GATGAG	1247
D6	1963	GATGAG	2018
RESULT 45			
AAX27906			
XX	AAX27906	Standard: DNA; 4963 bp.	
XX	AAX27906:		
XX	03 JUN 1999 (first entry)		
XX	Rabbit prostaglandin receptor under control of pMV*-1 promoter.		
DE	17A Transfection: tetraoffine controllable transactivator;		
XX	17B Expression regulation: tet operator-linked gene therapy;		
KW	cancer treatment; viral disease; pMV*-1 promoter;		
XX	prophylactic receptor; ds.		
OS	<i>cytotoxicus</i> sp.		
OS	Human cytomegalovirus.		
XX	US888981 A.		
XX	40 MAR 1999.		

[illegible]

QY 1075 GCTCTGATCAGACGATACGACGATGCT---GACAGACGACGACGATGCTGCTGCTGCTG 1141
 DB 1843 ACATTTCTCTCCAGTACGCTGAGTCTGTGGAGAGCAAGACCAATATCAAGAGACTG 1902
 QY 1132 AAGCGGATGACGAGATGCTTACCTTGGGATGATGACCAAGACGACATCTCTGACGAG 1191
 DB 1903 GACAAATATCAAGACGATTTATTCACCTGATGATGACCAAGACGACATCTGACGAG 1962
 QY 1192 CAATTCATGCTGCTGATTAACCTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1247
 DB 1963 CAGGACCAATGAGTGGGCTGAGCTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 2018

RESULT 38

ABL86920
 ID ABL86920 standard: cDNA: 2092 BP.

AAC86920:

AC 02-APP-2001 (first entry)

DE Nucleotide sequence of the human estrogen receptor cDNA

KM Ribozyme; estrogen dependent tumour; cell proliferation; glucocorticoid;

KM DNA-binding domain; estrogen receptor; cancer treatment; breast cancer;

KM ss.

OS Homo sapiens.

FN W0200074485-A1.

PD 14 DEC-2000.

PE 02-JUN-2000; 2000W0-US15243.

PR 04-JUN-1999; 9908-0137470.

PA (TEXAS) UNIV TEXAS.

PI Roy AK, Laretsky Y, Tyagi RK, Song GS, Chatterjee B.

WP1: 2001 06163307.

PT Ribozyme having a high substrate specificity for an mRNA encoding a

PT DNA binding domain of human estrogen receptor, useful for inhibiting a

PT estrogen dependent tumour cell proliferation, particularly breast cancer

PS Disclosure: Page 8-9; 4pp; English.

CC The specification describes a ribozyme capable of inhibiting

CC estrogen-dependent tumour cell proliferation and having a high

CC substrate specificity for an mRNA sequence encoding a DNA-binding

CC activity of human estrogen receptor. The ribozyme is free of endonuclease

CC treatment and therapies, especially for inhibiting estrogen-dependent

CC tumour cell proliferation, particularly breast cancer. The present

CC sequence represents the human estrogen receptor cDNA.

SU Sequence 2092 BP; 473 A; 605 C; 593 G; 421 T; 0 other;

Query Match 25.4%, Score 320.4, E-22, Length 2072;
 Host Local Similarity 60.6%; Pred. No. 3, 20-74;
 Matches 616; Conservative 0; Mismatches 361; Indels 39; Gaps 4;

DB 890 TGGCTCTGATGAGGCTGAGAGGCTCTGTAAGAGCAAGATATTCAAGATATAT 949
 QY 491 ATTGTTCAGACTACCAATAGTGTATCAATGATAAAGACGGGGAGAGATTCACAGG 450
 DB 950 ATGTGTGACAGCCAGCAAGTACGTGACATTTGATTAAGACAGAGAGAGAGAGAGAG 1009
 QY 451 TTTGAGTTCGAGATTTGATGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 510
 DB 1010 TTTGAGTTCGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 1069
 QY 511 TTTGAGTTCGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 558
 DB 1070 ATATGATGAGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 1129
 QY 559 CACTGTGCGGAG 607
 DB 1130 GTTGGGCTGCTGAG 1189
 QY 608 -----GGGAGCGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
 DB 1190 GTTGGGCTGCTGAG 1249
 QY 658 GTTGGGCTGCTGAG 714
 DB 1250 TTTGAGTTCGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 1309
 QY 715 GCTTCATGATGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
 DB 1410 GCTTCATGATGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369
 QY 775 TTTGAGTTCGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 834
 DB 1370 TTTGAGTTCGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAG 884
 QY 835 GAGAGCTGTGATGAG 894
 DB 1430 GAGAGCTGTGATGAG 1489
 QY 895 GAGAGCTGTGATGAG 954
 DB 1440 GAGAGCTGTGATGAG 1503
 QY 955 GAGAGCTGTGATGAG 1014
 DB 1550 GAGAGCTGTGATGAG 1609
 QY 1015 GAGAGCTGTGATGAG 1074
 DB 1610 GAGAGCTGTGATGAG 1669
 QY 1075 GAGAGCTGTGATGAG 1131
 DB 1670 GAGAGCTGTGATGAG 1729
 QY 1132 AAGAGCTGTGATGAG 1191
 DB 1730 AAGAGCTGTGATGAG 1789
 QY 1192 CAATTCATGCTGCTGATTAACCTTCGATGCTGCTGCTGCTGCTGCTGCTGCTG 1247
 DB 1790 CAATTCATGCTGCTGATTAACCTTCGATGCTGCTGCTGCTGCTGCTGCTG 1845

RESULT 39

ABL51900
 ID ABL51900 standard: cDNA: 2092 BP.

AAC51900:

AC 10-JUN-2002 (first entry)

DE Human estrogen receptor encoding cDNA SPO ID NO:9.

DB



Dy
1167 ACCGACCTTTTGGTTTGGATATTGGTAAGAGAGGAAATGTCTCTCAAGCAGGAATTTAATG 1178

Dz
1201 CGCGTCGCTAACTCTTGATATCTCTTATATCTTAACTAAGCATCTGAA 1247
TT
1227 GCGCTGGCTAACCTCTGATCTCTCTCTCCAGCTGAGGATATCTGAGG 1278

RESULT 2

US-09-139-617-2
Sequence 2, Application US/09139617
Patent No. 622015
GENERAL INFORMATION:
APPLICANT: WILKINSON, HILARY
TITLE OF INVENTION: ESTROGEN RECEPTOR
FILE REFERENCE: 20047Y
CURRENT APPLICATION NUMBER: US/09/139,617
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 60/058,271
EARLIER FILING DATE: 1997-09-08
EARLIER APPLICATION NUMBER: 60/060,520
EARLIER FILING DATE: 1997-03-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1647
TYPE: DNA
ORGANISM: HUMAN
US-09-139-617-2

```
Query Match      99.79; Score 1247, PB 4, Length 1647,
Best Local Similarity 100.00; P-Val No. 0;
Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible][illegible]

RESULT 3

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US-09-561-741A-2
Sequence 2, Application US/09561741A
Patent No. 6458551
GENERAL INFORMATION
APPLICANT: WILKINSON, HILARY
TITLE OF INVENTION: ESTROGEN RECEPTOR
FILE REFERENCE: 20047Y
CURRENT APPLICATION NUMBER: US/09/561,741A
CURRENT FILING DATE: 2000-04-26
PRIORITY APPLICATION NUMBER: us/01/49,617
PRIORITY FILING DATE: 1998-08-25
PRIORITY APPLICATION NUMBER: us/97/58,271
PRIORITY FILING DATE: 1997-09-08
PRIORITY APPLICATION NUMBER: us/96/05,420
PRIORITY FILING DATE: 1997-09-30
NUMBER OF SEQ IDS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1647
TYPE: DNA
ORGANISM: HUMAN
US-09-561-741A-2

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Query Match 99.79; Score 1247; DB 4; Length 1647;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1447; Conservative 0; Mismatches 0; Gaps 0;

[illegible]

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RESULT 19
US-08-076-726-15
: Sequence 15, Application US/08076726

GENERAL INFORMATION:

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APPL ("ANT" : (process), MainProc
APPL ("ANT" : MainProc,
APPL ("ANT" : MainProc,

```

TITLE OF INVENTION: Tight control of gene expression in
TITLE OF INVENTION: *Escherichia coli* by constitutive re-

NUMBER OF SPECIMENS: 16

ADDRESS: Stern, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, N.W.
CITY: Washington

STATE: District of Columbia
COUNTRY: United States of America

ZIP: 20005-3934

2. MEDIUM TYPE: Floppy disk

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COMPILER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS
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: SOTFWAKE: Patient in recovery
 :
 : CURRENT APPLICATION DATA:

ADDITIONAL INFORMATION: US/08/076, 726

PLANNING DATE: 14-JUN-1997
CLASSIFICATION: 445

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893
REFERENCE/BOOK NUMBER: 0942, 249000

THE JOURNAL OF THE AMERICAN MEDICAL ASSOCIATION
PUBLISHED WEEKLY
535 N. Dearborn St., Chicago, Ill. 60610-5412
Subscription Service Department
Second-class postage paid at Chicago, Ill.
Postmaster: Send address changes in U.S.A. to JOURNAL OF THE AMERICAN MEDICAL ASSOCIATION, 535 N. Dearborn St., Chicago, Ill. 60610-5412. Outside U.S.A.: The Journal of the American Medical Association, P.O. Box 179, Wellesley, Mass. 02158.
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Claims for missing issues will only be considered if made immediately on receipt of following issue.
Second-class postage paid at Chicago, Ill.
Postmaster: Send address changes in U.S.A. to JOURNAL OF THE AMERICAN MEDICAL ASSOCIATION, 535 N. Dearborn St., Chicago, Ill. 60610-5412. Outside U.S.A.: The Journal of the American Medical Association, P.O. Box 179, Wellesley, Mass. 02158.
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TEL/FAX: (202) 371-2540

```

;      FILL:      2488535, SSK
;
;      INP0KMAP1 (IN FOR SEQ 1) NO:      15;

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LENGTH: 6244 base pairs

TYPE: nucleic acid
STRANGLINGS: both

1. $\text{P}(\text{X} = 0) = 0.2$
 2. $\text{P}(\text{X} = 1) = 0.3$
 3. $\text{P}(\text{X} = 2) = 0.5$

1 12 / 1 / 0 00 30

Query Match	7.1k	Score 89, DB 1	Length 6244
Best Local Similarity	66.3k	Prod. No. 5, 10-14	

Matches	128;	Conservative	0;	Mismatches	65;	Indels	0;	Gaps	0;
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CTCAGTTCGACCCATTAAGCAATCGCATGCAGTCTGGTGTTGAAGCATGTAAAG

4742

2465, 1'CTTCTGGGATGAAAGATTACGCTGTATTATGGCTGCTCCACCTGTGGGAGCTGTAAAG 2474

353 6'CTTTTAAAGAA3'A1TC'AAGGACATATGAT1TATTTTGTCTCA3'CTACAAAT1A2T 412

Dbb 2425 TTTCTTAAAGGCGAATGCAAGGCGAGCTAACTATTATGTGCTGGAGAATGANT 2484

[illegible][illegible][illegible]

474 AACCTGGGCAATCGCT 485

Db 2545, AACCTTCTCTATCTT 2557

05 08 26:0 452 P

Sequence No. Application US/08260452
Patent No. 5650298


```

APPLICANT: Gosson, Manfred
APPLICANT: Hujard, Hermann
APPLICANT: Salfeld, Jochem
APPLICANT: Voss, Jeffrey
TITLE OF INVENTION: Animal transgenic for a tetracycline-controlled
NUMBER OF SEQUENCES: 10
CORRESPONDENT'S ADDRESS:
ADDRESS: Labiva & Gockleyd
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,970
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260,452
FILING DATE: 14-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,327
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/EXCERPT NUMBER: 841-013CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227 7480
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: human cytomegalovirus
STRAIN: Towne (hcmv)
IMMEDIATE SOURCE:
CLONE: pUHD BGR3
US-08-481-970-8

```

[illegible]

```

1 Patent No. 9,529,927
2
3 GENERAL INFORMATION:
4
5 APPLICANT: Gossen, Manfred
6
7 APPLICANT: Enjard, Hermann
8
9 APPLICANT: Salfield, Jochem
10
11 APPLICANT: Voss, Jeffrey
12
13 TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotic
14
15 TITLE OF INVENTION: Cells by Tetraacycline-responsive Promoters
16
17 NUMBER OF SEQUENCES: 10
18
19 CORRESPONDENT ADDRESS:
20
21 ADDRESSEE: Lathive & Cowpfield
22
23 STREET: 60 State Street
24
25 CITY: Boston
26
27 STATE: Massachusetts
28
29 COUNTRY: USA
30
31 ZIP: 02109-1875
32
33 COMPUTER READABLE FORM:
34
35 MEDIUM TYPE: Floppy disk
36
37 COMPUTER: IBM PC compatible
38
39 OPERATING SYSTEM: PC-DOS/MS-DOS
40
41 SOFTWARE: ASCII text
42
43 CURRENT APPLICATION DATA:
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45 APPLICATION NUMBER: US/08/897,719
46
47 FILING DATE:
48
49 CLASSIFICATION:
50
51 PRIOR APPLICATION DATA:
52
53 APPLICATION NUMBER: 08,740,452
54
55 FILING DATE:
56
57 APPLICATION NUMBER: 08/076,327
58
59 FILING DATE: 14-JUN-1994
60
61 ATTORNEY/AGENT INFORMATION:
62
63 NAME: Giulio A. DeConti, Jr.
64
65 REGISTRATION NUMBER: 31,503
66
67 REFERENCE/DOCKET NUMBER: BBI-0130P
68
69 TELECOMMUNICATION INFORMATION:
70
71 TELEPHONE: (617) 227-7400
72
73 TELEFAX: (617) 227-5941
74
75 INFORMATION FOR SEQ ID NO: 8:
76
77 SEQUENCE CHARACTERISTICS:
78
79 LENGTH: 6244 base pairs
80
81 TYPE: nucleic acid
82
83 STRANDEDNESS: double
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85 TOPOLOGY: circular
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87 MOLECULE TYPE: RNA (genomic)
88
89 ORIGINAL SOURCE:
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91 ORGANISM: Human cytomegalovirus
92
93 STRAIN: Towne (hCMV)
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95 IMMEDIATE SOURCE:
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97 CLONE: pUHD B6B3
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99 US-08-897-719-8

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[illegible]


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1 CLASSIFICATION: 435
2 ALI-BREV/ACENT INFORMATION:
3 NAME: KILL, Gordon
4 REGISTRATION NUMBER: 30,764
5 REFERENCE/JOCKET NUMBER: A-6612
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (202) 293-7060
8 TELEFAX: (202) 293-7860
9 INFORMATION FOR SEQ ID NO: 1:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 3014 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: cDNA
16 HYDROTHERICAL: NO
17 US-08-629-939-1
18
19 Query Match 6.5% Score 81: DB 1: Length 3014:
20 Best Local Similarity 63.7% Pred. No. 5,36-12:
21 Matches 129: Gaps 0: Mismatches 70: Indels 0: Gaps 0:
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[illegible]


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1 NUMBER OF SEQUENCES: 6
2 CORRESPONDENCE ADDRESS:
3 ADDRESS: COOPER & DUNHAM
4 STREET: 40 ROCKEFELLER PLAZA
5 CITY: NEW YORK
6 STATE: NEW YORK
7 COUNTRY: U.S.A.
8 ZIP: 10112
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: floppy disk
11 OPERATING SYSTEM: PC DOS/MS-DOS
12 SOFTWARE: Patent Release #1.24
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: PCT/US92/02120A
15 FILING DATE:
16 CLASSIFICATION:
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 6,75,084
19 FILING DATE: 22 MAR 1991
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 6,75,848
22 FILING DATE: 22 MAR 1991
23 ATTORNEY/AGENT INFORMATION:
24 NAME: WHITE, JOHN P.
25 REGISTRATION NUMBER: 28,678
26 REFERENCE/DOCKET NUMBER: 68694-POCT
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (212) 977 9550
29 TELEFAX: (212) 644 0525
30 TELETYPE: (212) 422524 (GPO) 01
31 INFORMATION FOR SEQ ID NO: 1:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 2928 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 IMMEDIATE SOURCE:
39 CLONING: BACAR ALPHA
40 FUNCTION:
41 NAME/KEY: GOS
42 LOCATION: 105-1488
43 OTHER INFORMATION:
44 PRT US92 02120A 4
45
46 Query Match 5.98; Score 74.4; DB 5; Length 2928;
47 Best Local Similarity 60.8%; Pctd. No. 2,90-10;
48 Matches 124; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
49
50 Y 286 TGGCTGTCTGAGCAATTAAGATGAGGATATGATGAGGCTGCTGCTGAGCA 445
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52 Db 664 TGGCTGTCTGAGCAATTAAGATGAGGATATGAGGCTGCTGCTGAGCA 424
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54 Y 446 TGTAAAGGCTTTTAAAGAAATGATTCAGACGATATGATATATTTGCTGAGTAA 405
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56 Db 424 TGTAAAGGCTTTTGTGCTGCTGAGATATGAGAAATGATGATGATACGCTGAGGAA 484
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58 Y 406 AATCACTGTAAATGATTAATAAAACCGGCAAGATGCTGAGGCTGCTGAG 465
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60 Db 484 AATCACTGTATATTAATTAATGAGGCTGAGGCTGAGGCTGAGGCTGAG 544
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62 Y 466 TGTATGAATGTGATGATGATGAG 489
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64 Db 544 TGTATGAATGTGATGATGATGAG 567
65
66 RESULT 34
67 US 08 592 484 1
68 Sequence 1. Application us-08-826-361a-2
69 Patent No. 5840760
70 GENERAL INFORMATION:
71 APPLICANT: Tsai, S. and S.J. Collins

```

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1 TITLE OF INVENTION: "Homotopologic Cell Lines Bearing Altered Retinoid Acid Re
2 NUMBER OF SEQUENCES: 10
3 CORRESPONDENCE ADDRESS:
4 ADDRESS: Christenson, O'Connor, Johnson and Kindness
5 STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
6 CITY: Seattle
7 STATE: Washington
8 COUNTRY: USA
9 ZIP: 98101
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette-5.25 inch, 1.2MB storage
12 OPERATING SYSTEM: MS-DOS 4.01
13 SOFTWARE: Word for Windows 5.01-t
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/592,483
16 FILING DATE:
17 CLASSIFICATION: 435
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/099,242
20 FILING DATE: July 28, 1994
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Broderick, Thomas F.
23 REGISTRATION NUMBER: 31,432
24 REFERENCE/DOCKET NUMBER: PCHR-1-7190
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 2940 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: double
32 TOPOLOGY: linear
33 MOLECULE TYPE: cDNA to mRNA
34 DESCRIPTION: see Figure 16B; RAR-alpha
35 IMMEDIATE SOURCE:
36 LIBRARY: cDNA
37 US-08-592-483-1
38
39 Query Match 5.98; Score 74.4; DB 2; Length 2940;
40 Best Local Similarity 60.8%; Pctd. No. 2,90-10;
41 Matches 124; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
42
43 Y 286 TGGCTGTCTGAGCAATTAAGATGAGGATATGATGAGGCTGCTGCTGAGCA 445
44 ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
45 Db 664 TGGCTGTCTGAGCAATTAAGATGAGGATATGAGGCTGCTGCTGAGCA 424
46
47 Y 446 TGTAAAGGCTTTTAAAGAAATGATTCAGACGATATGATATATTTGCTGAGTAA 405
48 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
49 Db 424 TGTAAAGGCTTTTGTGCTGCTGAGATATGAGAAATGATGATGATACGCTGAGGAA 484
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53 Db 484 AATCACTGTATATTAATTAATGAGGCTGAGGCTGAGGCTGAGGCTGAG 544
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55 Y 466 TGTATGAATGTGATGATGATGAG 489
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57 Db 544 TGTATGAATGTGATGATGATGAG 567
58
59 RESULT 35
60 5171671 1
61 Patent No. 5171671
62 APPLICANT: EVANS, RONALD M.;ONG, ESTELITA S.;SEBOLD,
63 PRUDHOMAR S.;THOMPSON, CATHERINE C.;DEMSON, KAZUHIKO
64 GIERHRE, VINCENT
65 TITLE OF INVENTION: RETINOIC ACID RECEPTOR COMPOSITION
66 NUMBER OF SEQUENCES: 2
67 CURRENT APPLICATION DATA:
68 APPLICATION NUMBER: 05/37,546, 256
69 FILING DATE: 06 AUG 1990
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER: 276, 546

```


[illegible]

RESULTS

US 08 312A 1/1

Patent No. 5,550,024

GENERAL INFORMATION

APPLICANT:	Rothschild, Max F.
APPLICANT:	Tingler, Christopher K.

APPLICANT: Jacobson, Carol D.

APPLICANT: Mileham, Alan J.
APPLICANT: Plastow, Graham S.

; APPLICANT: Vaske, David

7 TITLE OF INVENTION: (See

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarloy, MCK

STREET: 801 Grand South
CITY: Los Angeles

STATE: Iowa

COUNTRY: United States
 TITLE: Editor

COMPILED BY: J. L. ...

SOFTWARE: Patent In Release #1.0, Version #1.000

CURRENT APPLICATION DATA: 115/008/312 3124

FILED IN DATE: 26 SEP 1994

CLASSIFICATION: 445
CONTROL: STUDY SECTION DATA

APPL. NO. 07/961,819

FILED DATE: 19 OCT - 1992

APPLICATION NUMBER: 115 074687-7006

FILED IN: DATE: 19-APR-1991

ATTORNEY/ACCIDENT INFORMATION:

NAME: MICHEL, HUGO S.
REGISTRATION NUMBER: 37,719

КОНТАКТЫ: 8(905) 4
11-11-11

TELECOMMUNICATION INFORMATION: 515-288-3667

TELEFAX: 515-288-1338

INFORMATION FOR SEO ID NO: 1:
SPOILING CHARACTERISTICS:

1. ENGLISH: 3460 base pairs

TYPE: modernized

: SIMPLICITY: GOOD!
 :
 : TOPOLOGY: I need

MOLECULAR TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO


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1 STRANDEDNESS: single
2 TOPOLOGY: linear
3 MOLECULE TYPE: cDNA
4 HYPOHETICAL: NO
5 ANTI-SENSE: NO
6 FEATURE:
7 NAME/KEY: misc_feature
8 LOCATION: 1..3511
9 OTHER INFORMATION: /function= "PM1-RAR" DNA Sequence."
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94 64.8 5.2 1404 10 US-09-965-704-62 Sequence 62, Appl
94 64.8 5.2 2711 10 US-09-952-559-2 Sequence 2, Appl
95 64.4 5.1 481 10 US-09-864-761-1645 Sequence 1645, A
96 64 5.1 430 9 US-09-918-995-42194 Sequence 42194, A
97 62.2 5.0 549 9 US-09-991-946-1417 Sequence 1417, Ap
98 6.2 5.0 1759 10 US-09-962-446-4300 Sequence 400, Ap
99 6.2 5.0 5642 12 US-10-002-600-54 Sequence 54, Appl
100 60.8 4.9 198 10 US-09-965-704-41 Sequence 41, Appl
101 60.8 4.9 1247 10 US-09-965-704-70 Sequence 70, Appl
102 60.8 4.9 1288 10 US-09-965-704-1 Sequence 1, Appl
103 60.8 4.9 1290 10 US-09-965-697-4 Sequence 4, Appl
104 60.8 4.9 1542 10 US-09-965-704-58 Sequence 58, Appl
105 60.8 4.9 2005 12 US-10-142-474-1 Sequence 1, Appl
106 60.4 4.8 9847 10 US-09-965-704-21 Sequence 21, Appl
107 60.4 4.8 1398 10 US-09-909-672-1 Sequence 1, Appl
108 60.2 4.8 2511 10 US-09-919-497-36 Sequence 36, Appl
109 60 4.8 492 9 US-10-052-092-4 Sequence 4, Appl
110 60 4.8 1237 9 US-10-052-092-4 Sequence 4, Appl
111 58.8 4.7 1463 9 US-09-918-995-15693 Sequence 15693, A
112 58.8 4.7 1740 9 US-10-161-804-26 Sequence 26, Appl
113 57 4.6 2751 10 US-09-728-422-2 Sequence 2, Appl
114 56 4.5 486 10 US-09-918-995-13740 Sequence 13740, A
115 56 4.5 1123 10 US-09-965-704-26 Sequence 26, Appl
116 55.8 4.5 2066 10 US-09-895-840-1 Sequence 1, Appl
117 55.8 4.5 2125 9 US-10-295-370-1 Sequence 1, Appl
118 55.2 4.4 571 9 US-10-066-543-458 Sequence 458, App
119 55.2 4.4 1847 9 US-10-295-370-4 Sequence 4, Appl
120 54.6 4.4 1484 10 US-09-731-557A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-198-785 1
? Sequence 1, Application US/10198785
? Publication No. US2003002224A1
? GENERAL INFORMATION:
? APPLICANT: OLIMPUS OPTICAL CO., LTD.
? TITLE OF INVENTION: Method of detecting binding reaction between protein and test sub
? FILE REFERENCE: 7E1-02S0548
? CURRENT APPLICATION NUMBER: US/10198-785
? CURRENT FILING DATE: 2002-07-19
? PRIOR APPLICATION NUMBER: JP/2001-220444
? PRIOR FILING DATE: 2001-07-17
? PRIOR APPLICATION NUMBER: JP/2001-221963
? PRIOR FILING DATE: 2001-07-24
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 1
? LENGTH: 1740
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: c155
? LOCATION: (99)-(1688)
US-10-198-785 1

Query Match 99.78% Score 1247; DB 9; Length 1740;

Best Local Similarity 100.0%; Prod. No. 0;

Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATATACAGATATGAGAAATGAGCTAACTTGAAGAGTGGGCTGCTGGAGAGAG 60
Db 1 ATGATATACAGATATGAGAAATGAGCTAACTTGAAGAGTGGGCTGCTGGAGAGAG 60
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QY 61 ACAAATCAAAATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 120
Db 111 ACAAATCAAAATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 120
Db 418 ACAAATCAAAATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 477
QY 121 CAACTATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 180
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QY 181 CAATATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 240
Db 438 CAATATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 497
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Db 498 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 557
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Db 558 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 617
QY 461 AAAAAAGATATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 420
Db 618 AAAAAAGATATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 677
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Db 678 GATAAAAAGATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 737
QY 481 ATGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 540
Db 748 ATGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 797
QY 541 ACTGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 600
Db 798 ACTGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 857
QY 601 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 660
Db 858 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 917
QY 661 GAGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 720
Db 918 GAGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 977
QY 721 ATGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 780
Db 978 ATGATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1037
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Db 1038 AAAAAAGATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1097
QY 841 TGTGATGATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 900
Db 1098 TGTGATGATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1157
QY 901 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 960
Db 1158 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1217
QY 961 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1020
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QY 1021 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1080
Db 1278 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1337
QY 1081 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1140
Db 1338 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1397
QY 1141 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1200
Db 1398 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1457
QY 1201 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1247
Db 1458 CAAATCAATGATGATGAGTAAACATGAGCTGAGTCTGCTTAACTGATCAATCA 1504

[illegible]

Dh 1258 CCGTCTAAGGAAATAAAGGCTTCTT

Eb	1198	GTGAGTTTGTGTAATACATACAGACTTCTTAATTGATGTAACGCTCTATGACAA	1257
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608 -----GGAGCTGCTGTCGAGCGCGCTGAACCGCGACAGCTAGTGTCTACCGTC 657

? TITLE OF INVENTION: Lipids
 ? FILE REFERENCE: 24799
 ? CURRENT APPLICATION NUMBER: US/10/259,864
 ? CURRENT FILING DATE: 2002-09-30
 ? PRIOR APPLICATION NUMBER: US 60/425,178
 ? PRIOR FILING DATE: 2001-09-28
 ? NUMBER OF SEQ ID NOS: 6
 ? SOFTWARE: Patent In version 3.1
 ? SEQ ID NO 4
 ? LENGTH: 3400
 ? TYPE: DNA
 ? ORGANISM: Rat/human chimera
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: (1)-(3400)
 ? OTHER INFORMATION:
 US 10-259,864-3

Query Match 19.0%; Score 248; DB 9; Length 3400;

Host Local Similarity 55.7%; Pred. No. 3,20-63;

Matches 554; Conservative 0; Mismatches 410; Indels 29; Gaps 4;

QY 284 TCTGCGTGTGAGCAATTAACGATCGGATATGAGCTGCTGCTGCAAG 343
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2075 TCTGCGGCTGTGCTGCTGATGAAAGCTTCAGATGCTATTCGCGCTGCAATGCGAA 2134
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 444 GATCTAAAGCGCTTTTAAAGACAGCATTCAGAGCAATATGATTAATTTGTCAGCTA 403
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2135 GCTGCAAGATATTCTTTAAAGACAGCAATGTAAGAGCAATTAATTAATTTGTCAGAA 2194
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 404 CAATTAAGTGTAAATATTAATAAAGCAAGGAGTTCGAGCGCTGCTGCAAGTTCGCA 463
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2195 CAATTAAGTGTCAATATTAATAAAGCAAGGAGTTCGAGCGCTGCTGCAAGTTCGCA 2254
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 464 AGCTTACAGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 523
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2255 AATGCTTACAGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2314
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 524 TCTGCTGAGCAATGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 583
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2415 TCTGCTGAGCAATGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2473
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 584 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 633
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2474 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2433
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 634 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 693
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2434 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2493
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 694 -----GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 738
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2494 TATCTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2553
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 739 AATCTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 798
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2554 AATCTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2613
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 799 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 858
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2614 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2673
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 859 AATCTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 918
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2674 AATCTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2733
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 919 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 978
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2734 TTTGCTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2793
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 979 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 1038
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 2794 GTCGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCA 2853
 1111 1111 1111 1111 1111 1111 1111 1111

RESULT 22

US-09-853-033-3

? Sequence 3; Application US/09853033

? Patent No. US20020100068A1

? GENERAL INFORMATION:

? APPLICANT: CHAMBER, PIERRE

? APPLICANT: METZGER, DANIEL

? TITLE OF INVENTION: TRANSDUCING MOUSE FOR TARGETED RECOMBINATION

? FILE REFERENCE: 065691/0222

? CURRENT APPLICATION NUMBER: US/09/853,033

? PRIOR FILING DATE: 2001-05-11

? PRIOR APPLICATION NUMBER: FR 00/12570

? NUMBER OF SEQ ID NOS: 14

? SOFTWARE: Patent In Ver. 2.1

? SEQ ID NO 3

? LENGTH: 1983

? TYPE: DNA

? ORGANISM: Artificial sequence

? FEATURE:

? NAME/KEY: CDS

? OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence

? OTHER INFORMATION: Homosapiens-Bacteriophage p1

US-09-853-033-3

Query Match 17.5%; Score 218.4; DB 10; Length 1983;

Host Local Similarity 61.5%; Pred. No. 3,10-57;

Matches 386; Conservative 0; Mismatches 236; Indels 6; Gaps 2;

QY 626 GCTTAAAGCTGAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1121 GCTTAAAGCTGAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1180
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 686 TCTTAAAGCTGAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 742
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1181 GCTTAAAGCTGAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 743 TGGGCAAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAG 802
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1241 TGGGCAAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAG 1300
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 803 AGCTGAGCTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAG 862
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1301 AGCTGAGCTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAG 1360
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 863 TGGGCAAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAG 922
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1361 TGGGCAAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAG 1420
 1111 1111 1111 1111 1111 1111 1111 1111
 QY 923 TCTGAGCAAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAG 982
 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1421 TCTGAGCAAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAG 1480
 1111 1111 1111 1111 1111 1111 1111 1111

FILE REFERENCE: TSRI 725.1

CURRENT APPLICATION NUMBER: US-09/908,153H
 CURRENT FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: US 09/619,063
 PRIOR FILING DATE: 2000-07-18
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 49
 LENGTH: 2739
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Synthesized
 US-09-908-153H-49

Query Match 16.1% Score 200.8; DP 9; Length 2739;
 Best Local Similarity 61.7%; Pred. No. 1,1e-51;
 Matches 338; Conservative 0; Mismatches 207; Indels 4; Gaps 1;

QY 703 CCCTTACCAACACCTCTATGATGATGAGCAATGGGCAAAAGAAATGGGA 762
 DB 748 CCTTATGTAAGCTGTAATGATGCTTATTACAACTTATGATGATGATG 807
 QY 763 CACATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAGAAA 822
 DB 808 CATATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAGAAA 867
 QY 823 GTCGAGCTTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAGTCAATCT 882
 DB 868 GTTCATCTTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAGTCAATCT 927
 QY 883 ATTACCAACACCTCTATGATGATGAGCAATGGGCAAAAGAAATGGGA 942
 DB 928 ATGCAACACCTCTATGATGATGAGCAATGGGCAAAAGAAATGGGA 987
 QY 943 AAATGCTCAAGAGATTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAG 1002
 DB 988 AAATGCTCAAGAGATTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAG 1047
 QY 1003 CAGATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1062
 DB 1048 CATATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1107
 QY 1063 TCCATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1122
 DB 1108 TCCATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1177
 QY 1123 CAGCTTCCGAGCGGGGAGAGCAATGGGCTTTGAGAGTCAATCTTTGAG 1179
 DB 1168 CAGCTTCCGAGCGGGGAGAGCAATGGGCTTTGAGAGTCAATCTTTGAG 1227
 QY 1180 TCCATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1246
 DB 1228 ATCTGATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1293
 QY 1249 CAGGCGAG 1247
 DB 1288 CACATGAG 1295

RESULT 31
 US-09-908-153H-44/7
 Sequence 44, Application US/09/08153H
 Patent No. US20020168714A1
 GENERAL INFORMATION:
 APPLICANT: Barbas, Carlos F.
 APPLICANT: Beertl, Roger
 APPLICANT: Schopfer, Ulrich
 TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
 TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
 FILE REFERENCE: US 725.1
 CURRENT APPLICATION NUMBER: US-09/908,153H
 CURRENT FILING DATE: 2001-07-18

CURRENT APPLICATION NUMBER: US 09/619,063
 PRIOR FILING DATE: 2000-07-18
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 44
 LENGTH: 2739
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Synthesized
 US-09-908-153H-44

Query Match 16.1% Score 200.8; DP 9; Length 2739;
 Best Local Similarity 61.7%; Pred. No. 1,1e-51;
 Matches 338; Conservative 0; Mismatches 207; Indels 4; Gaps 1;

QY 703 CCCTTACCAACACCTCTATGATGATGAGCAATGGGCAAAAGAAATGGGA 762
 DB 748 CCTTATGTAAGCTGTAATGATGCTTATTACAACTTATGATGATGATGATG 807
 QY 763 CACATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAGAAA 822
 DB 808 CATATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAGAAA 867
 QY 823 GTCGAGCTTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAGTCAATCT 882
 DB 868 GTTCATCTTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAGTCAATCT 927
 QY 883 ATTACCAACACCTCTATGATGATGAGCAATGGGCAAAAGAAATGGGA 942
 DB 928 ATGCAACACCTCTATGATGATGAGCAATGGGCAAAAGAAATGGGA 987
 QY 943 AAATGCTCAAGAGATTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAG 1002
 DB 988 AAATGCTCAAGAGATTTGAGAGTGGGCTTTGAGAGTCAATCTTTGAGAG 1047
 QY 1003 CAGATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1062
 DB 1048 CATATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1107
 QY 1063 TCCATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1122
 DB 1108 TCCATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1177
 QY 1123 CAGCTTCCGAGCGGGGAGAGCAATGGGCTTTGAGAGTCAATCTTTGAG 1179
 DB 1168 CAGCTTCCGAGCGGGGAGAGCAATGGGCTTTGAGAGTCAATCTTTGAG 1227
 QY 1180 TCCATATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1246
 DB 1228 ATCTGATATAGTGGGCAAGAGATGGGCTTTGAGAGTCAATCTTTGAG 1293
 QY 1249 CAGGCGAG 1247
 DB 1288 CACATGAG 1295

RESULT 32
 US-09-908-153H-41
 Sequence 41, Application US/09/08153H
 Patent No. US20020168714A1
 GENERAL INFORMATION:
 APPLICANT: Barbas, Carlos F.
 APPLICANT: Beertl, Roger
 APPLICANT: Schopfer, Ulrich
 TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
 TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
 FILE REFERENCE: US 725.1
 CURRENT APPLICATION NUMBER: US-09/908,153H
 CURRENT FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: US 09/619,063
 PRIOR FILING DATE: 2000-07-18

ORGANISM: Homo sapiens
US-09-962-446-268

Query Match 10.7% Score 133.8 DB 10 Length 2188
Best Local Similarity 49.9% Prod No 7 36-31
Matches 482: Conservative 0: Mismatches 482: Indels 6: Gaps 2:

```

UY 280 CATTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
DB 406 GCTCTGCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 440 GAAGATGTAAGGCTCTTTTAAAGATATGATGATGATGATGATGATGATGATGATGATGAT
DB 466 GAGGCTGTAAGGCTCTTTTAAAGATATGATGATGATGATGATGATGATGATGATGATGAT
UY 400 GCTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 526 GCTCCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 460 GCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 586 ACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 520 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
DB 646 GAGGCTGTAAGGCTCTTTTAAAGATATGATGATGATGATGATGATGATGATGATGATGAT
UY 580 AATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 706 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 640 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 766 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 700 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
DB 826 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 760 GCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 883 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 820 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 943 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 880 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 1003 TCACTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 940 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 1060 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 1000 TTTGAGAGTTAAAGTCCAGACAAAGAAATATCTGTGTGATGATGATGATGATGATGAT
DB 1120 GTCAGAGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 1060 AATTC 1064
DB 1180 AATTC 1184

```

RESULT 35
US-10-211-239-7
Sequence 7, Application US/10211239
Publication No. US2003010365A1
GENERAL INFORMATION:
APPLICANT: Jung, Bitgit
APPLICANT: Kraft, No. US2003010365A1
APPLICANT: Mueller, Stefan
TITLE OF INVENTION: Method for Identifying Substances Which Positively

TITLE OF INVENTION: Influence Inflammatory Conditions
FILE REFERENCE: 0652,246001
CURRENT FILING DATE: 2002-08-05
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 60/415,775
PRIOR APPLICATION NUMBER: EP 01119003.0
PRIOR FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patented version 3.1
SEQ ID NO 7
LENGTH: 2402
TYPE: DNA
ORGANISM: Homo sapiens
US-10-211-239-7

```

Query Match 10.7% Score 129 DB 9 Length 2402
Best Local Similarity 48.7% Prod No. 2 46-29
Matches 482: Conservative 0: Mismatches 400: Indels 5: Gaps 1:

UY 280 CATTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
DB 583 GCTCTGCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 340 GAAGATGTAAGGCTCTTTTAAAGATATGATGATGATGATGATGATGATGATGATGATGAT
DB 643 GAGGCTGTAAGGCTCTTTTAAAGATATGATGATGATGATGATGATGATGATGATGATGAT
UY 400 GCTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 703 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 460 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 763 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 520 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
DB 823 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 580 AGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 883 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 640 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 943 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 700 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
DB 1003 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 760 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 1063 GCTCTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 820 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 1123 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 880 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 1183 TCACTGCTGCTGTGTGAGCCATTAGCATGCGATATGCTATGAGTATGAGTGTGCTGT
UY 940 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 1240 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 1000 TTTGAGAGTTAAAGTCCAGACAAAGAAATATCTGTGTGATGATGATGATGATGATGAT
DB 1300 GTCAGAGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
UY 1060 AATTC 1064

```


DB 1826 AAGCAGGAGTACTGTGGAGCCCGGAGGTTAAAGAACTGGGAATCTCAACTGGAA 1885
541 GAGATATAGAAATTTCTGATAGAGCAATCTGACTGTGGGCGCAAGGCAAGAAATGGGCG 530
DB 1886 AGCAATGATAGAACTTTCAATCTTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1445
591 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 640
DB 1946 TGTCAACATTTGAGAGGATATAGAGT-----TCAAGCCATCTTCTGAAATGTC 1992
651 GAGCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 710
DB 1949 GTTAAAGGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2051
671 GAGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
DB 2052 GTTAAAGGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2111
771 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 830
DB 2112 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2171
831 GTTAAAGGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 884
DB 2172 GATTAAGGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2231
885 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 926
DB 2232 GATTAAGGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2273

RESULT 38

US-09-997-267-1
Sequence 1, Application US/09997267
Patent No. US20020165481A1
GENERAL INFORMATION:
APPLICANT: AHRENS-FATH, ISABELLE
APPLICANT: HAENDLER, BERNARD
TITLE OF INVENTION: HUMAN ANDROGEN RECEPTOR VARIANTS
FILE REFERENCE: SCH-1793
CURRENT APPLICATION NUMBER: US-09-997-267
PRIORITY FILING DATE: 2001-11-30
PRIORITY FILING DATE: 2000-12-14
NUMBER OF SEQ IDS NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 1
LENGTH: 1326
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-267-1

Query Match 7.6% Score 95.2 DB 9% Length 1326
Best Local Similarity 51.2% Pctd. No. 5,80-192
Matches 332: Conservative 0: Mismatches 298: Indels 18: Gaps 4:
DB 243 GTGCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 302
445 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404
DB 403 GTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 462
405 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 464
DB 463 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 422
465 GTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524
DB 423 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482

QY 525 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 584
DB 484 ACTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541
QY 545 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 644
DB 542 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 591
QY 645 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 704
DB 592 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 650
QY 705 GTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764
DB 651 GAGCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 710
QY 765 GATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 824
DB 711 GTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 770
QY 825 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 878
DB 771 GATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 830
QY 879 GTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 926
DB 831 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 878

RESULT 39

US-09-880-107-2300
Sequence 2400, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, David T.
APPLICANT: Voelkel, Joseph G.
APPLICANT: Scherf, Dwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-MO
CURRENT APPLICATION NUMBER: US/09/880,107
PRIORITY FILING DATE: 2001-06-14
PRIORITY FILING DATE: 2000-06-14
PRIORITY FILING DATE: 2000-10-02
NUMBER OF SEQ IDS NOS: 3950
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 2400
LENGTH: 4715
TYPE: DNA
ORGANISM: Homo sapiens
OTHER INFORMATION: Genebank Accession No. US20020142981A1 M24563
US-09-880-107-2400

Query Match 7.6% Score 95.2 DB 10% Length 4715
Best Local Similarity 51.2% Pctd. No. 1e-18
Matches 332: Conservative 0: Mismatches 298: Indels 18: Gaps 4:
QY 285 GTGCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 444
DB 2202 GTGCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2261
QY 445 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404
DB 403 GTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 462
405 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 464
DB 463 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 422
465 GTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524
DB 423 AAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482

GenCore version 5.1.6
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us-08-826-361a-2.rst

Run on: June 15, 2003 21:08:27 Search time: 1903.92 seconds
(without alignments)
10641 499 Million cell operations/sec

Title: US-08-826-361a-2

Project score: 1251

Sequence: 1 AAGATTACAGCATTCCTGAG AATTCAGCATTCCTGAG (1251)

Scoring table:

IDENTITY_MTC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743476 residues

Total number of hits satisfying chosen parameters: 32308142

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database:

EST:
1: em_est1a.*
2: em_est1b.*
3: em_est1c.*
4: em_est1d.*
5: em_est1e.*
6: em_est1f.*
7: em_est1g.*
8: em_est1h.*
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26: em_est1z.*
27: em_est1aa.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	155.4	12.4	641	10	us-08-826-361a-2
5	153.8	12.3	648	12	us-08-826-361a-2
6	149.6	12.0	642	12	us-08-826-361a-2

7	143.4	11.5	627	14	us-08-826-361a-2
8	143.2	11.4	782	10	us-08-826-361a-2
9	131.4	10.5	594	12	us-08-826-361a-2
10	129.8	10.4	1142	14	us-08-826-361a-2
11	126.4	10.1	137	17	us-08-826-361a-2
12	117	9.4	692	13	us-08-826-361a-2
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19	107.4	8.5	2199	11	us-08-826-361a-2
20	106.2	8.5	626	12	us-08-826-361a-2
21	102	8.2	844	13	us-08-826-361a-2
22	101.4	8.1	937	13	us-08-826-361a-2
23	100.4	8.0	558	13	us-08-826-361a-2
24	99.8	8.0	908	10	us-08-826-361a-2
25	99.6	8.0	800	9	us-08-826-361a-2
26	99.6	8.0	1004	9	us-08-826-361a-2
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28	96.6	7.7	775	12	us-08-826-361a-2
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c	82	85.2	6.8	64.5	10	HE5.4846
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c	84	85	6.8	91.0	9	AL5.56.30.2
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c	86	84.8	6.8	44.5	12	HE55.1955
c	87	84.8	6.8	984	9	AAR51.319
c	88	84.8	6.8	984	9	AAR9.618
c	89	84.8	6.8	490	14	W1.715
c	90	84.8	6.8	428	9	AL.42.94.3
c	91	84.8	6.8	451	9	AL.42.74.3
c	92	84.8	6.8	500	10	AW490.389
c	93	84.8	6.8	574	9	AL12.71.21
c	94	84.8	6.8	588	10	AA4910.78
c	95	84.8	6.8	655	10	AV64.7680
c	96	84.8	6.8	96.3	14	HQ9.606.3
c	97	84.2	6.7	466	9	AA744.444
c	98	84.2	6.7	410	14	HQ94.92.9
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c	116	82.2	6.6	584	12	HE.32.8.3.1.2
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c	82	85.2	6.8	64.5	10	HE5.4846
c	83	85.2	6.8	94.7	9	AL5.27466
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c	116	82.2	6.6	584	12	HE.32.8.3.1.2
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A1.1 (MIN)S

RESULT 1	66722442	727 bp	mRNA	Heart	EST 38 MAY 2002
LOCUS	66722442				
DEFINITION	mRNA for p115 N1H_MGC_97 Homo sapiens cDNA clone IMAGE445947.5.				
ACCESSION	66722442				
VERSION	66722442.1				
KEYWORDS	EST.				
SOURCE	Human.				
ORGANISM	Homo sapiens				
REFERENCE	Eskuriot; Metazo; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchonta; Primates; Carnivora; Homidae; Homo 1 (bases 1 to 727)				
AUTHORS	N1H MGC http://image.ncbi.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	<p>Unpubl. (1999)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: carp@fsl.rii.nih.gov</p> <p>Tissue Procurement: Miklos Patkows, M.D., Ph.D.</p> <p>cDNA Library Preparation: Michael J. Brownstein (NIGR), Shiroki Toshiyuki and Piero Carnini (RIKEN)</p> <p>cDNA Library Arrayed by: The T.M.A.G.E. Consortium (TMNL)</p> <p>TMNL Sequencing by: Incyte Genomics, Inc.</p> <p>Clone distribution by: MGC clone distribution information can be found through the T.M.A.G.E. Consortium (TMNL) at:</p> <p>http://imayc.tlnl.gov</p>				
PLATES	U1A010759	row: n	column: 18		

Hrb quality sequence style 725.

Location/Qualifiers

1..727

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/db_xref="taxon:9606"

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/note="Organ: testis; Vector: phagescript R(+); Site_1: BamHI; Site_2: SalI; XhoI (at cagcag); oligo-dt primed using primer 5' TTTTCTTTTTTTTTC-3'; size selected for average insert size 2.2 kb and normalized to ref 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Garinich, in preparation). Library constructed by M. Brownstein (NIH/NIDDK, National Institutes of Health). Note: this is a NIH-MGC library."

BASE COUNT

182 a 194 c 175 g 176 t

ORIGIN

Genety Match: 21.0% Score 262.4; pos 12; Length 727;

Best Local Similarity: 99.3%; Pred. No.: 1.2e+64; Indels 1; Gaps 1;

Mutations: 274; Conserved: 0; Mismatches 1;

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UY 61 ACAAATCAAAATGTTGT 120
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DB 511 AACAAATCAAAATGTTGT 570
UY 121 CACTTATCAATCCTGATGCGAAATCTGAAAAGAGTCTGTGTTTGAAGCAATCATCTATA 180
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DB 571 CAGTATCAATCCTGATGCGAAATCTGAAAAGAGTCTGTGTTTGAAGCAATCATCTATA 640
UY 181 CAACACACCTTACCTGTAAACACACACACACCTGAAAA GCAGACTTACCTGGCAACCTCTTC 240
|||||
DB 641 GAACACACCTTACCTGTAAACACACACACACCTGAAAA GCAGACTTACCTGGCAACCTCTTC 690
UY 243 TACCAAGCTCTCTATCTACTCTTACCTGTAAACACACAC 275
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DB 691 CTCACAGCTCTCTATCTACTCTTACCTGTAAACACACAC 726

RESULT 2

B6748148 580 bp mRNA linear EST 15 MAY 2001

LOCUS B6748148

DEFINITION B6748148 zebrafish atrial-ventricular junctional cDNA clone ZF8705

VERSION B6748148

FEATURES

SOURCE

ORGANISM zebrafish.

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 580)

Clark,M., Johnson,S.L., Jachrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Korda,L., Martin,D., Monk,T., Myhre,T., Underwood,K.R., Stepien,B., Theisinger,B., Allen,M., Bowser,Y., Peterson,B., Swadlow,T., Gibbons,M., Pappe,D., Harvey,N., Schumaker,K., Kittler,E., Kolm,S., Shiao,T., Jackson,Y., Cardenas,M., McManis,R., Waterston,R. and Wilson,R.

WASB Zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: U04105.x1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, box 8501, St. Louis, MO 63110, USA

Tel: 314 286 1800

Fax: 314 286 1810

TITLE
RIKEN MOUSE ESTS (Kono, H., et al.)
Tsumoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamada, I.,
Yano, F., Yasunishi, A., Yokota, I., Yoshida, K., Yoshiki, A., Yoshino
M., Muratsu, M. and Hayashizaki, Y.

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1-7-23 Suehira-cho, Tsutsumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: yoneome-res@sci.riken.go.jp

Ushida, H., Ogawa, T., Kono, G., Ito, H., Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermostabilization and thermoinactivation of thermolabile enzymes by

CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itchh.M., Kitsuai,T., Akiyama,J., Shibata,K., Iwaw,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

Automated filtration-based high-throughput plasmid preparation system (Genome Res. 5), 464-470 (1995)

19-44 (1999)
please visit our web site (<http://genome.rri.riken.go.jp>) for further details.
location/qualifiers

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/db_xref="taxon:10090"
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/lab_post="DH10B"
/note="Site_1: Salt; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Flycatcher
Project of Genome Research Center, Osaka Univ."

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Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15'

68AAGACATGAAATTTTAAAGACCTCCTTTTTTTTTTTTTTTTAA 31, cDNA was prepared by using trehalose thermo activated reverse transcriptase and subsequently enriched for full-length by CAP-trapper. cDNA went through one round of normalization

strand cDNA was prepared with the primer adaptor sequence [5'-GAGAGAGACATTTTCAGATTAAATAATTTTTTGGCC-3']. cDNA was cleaved with XhoI and BamHI. Vector, a

	FLC I. "			
BASE COUNT	75 a	65 c	68 g	67 t
ORIGIN				

Query Match:	7.28;	Score	89.5;	DE	19;	Length	275;
Fast local Similarity	64.4%;	Pred No	8	30-15;			
Matches	134;	Conservative	0;	Mismatches	74;	Indels	0;
				Gaps			0;

[illegible]

Db 114 GTGTGTAATCTTTAAATTAAGTAAAGGAAATACCAATTAACCTTTC 173

GenCore version 5.1.6
Copyright (c) 1998 - 2003 CompuGen Ltd.

1M protein - protein search, using SW model

Run on: June 16, 2003, 03:20:57 : Search time 125.704 seconds

(without alignment)
505,642 Million total updates/sec

Title: US-08-826-361a-5

Perfect score: 2522

Sequence: 1 MYVSLPSNVTNLFKPGPGQT PPSVAFPSKSPGSGNPGSG 477

Scoring table:

Matrix: BLOSUM62

Gap: 10.0, Gapext: 0.5

Searched: 908470 seqs, 13350620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 120 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No	Score	Query Match	Length	DB	ID	Description
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4	2522	100.0	477	23	AAW14725	Human oestrogen re
5	2522	100.0	477	23	AAW14726	Human oestrogen re
6	2522	100.0	477	23	AAW14727	Human oestrogen re
7	2522	100.0	477	23	AAW14728	Human oestrogen re
8	2522	100.0	477	23	AAW14729	Human oestrogen re
9	2522	100.0	477	23	AAW14730	Human oestrogen re
10	2522	100.0	477	23	AAW14731	Human oestrogen re

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13	2257	89.5	439	20	AAW04812	Human oestrogen re
14	2255	89.4	549	20	AAW04434	Human oestrogen re
15	2249	89.2	485	18	AAW14723	Human oestrogen re
16	2249	89.2	485	18	AAW01596	Human oestrogen re
17	2246	88.7	567	20	AAW098128	Human oestrogen re
18	2231.5	88.5	474	21	AAW19346	Human oestrogen re
19	2230	88.4	485	18	AAW14725	Human oestrogen re
20	2212	87.7	460	20	AAW04434	Human oestrogen re
21	2198	87.2	416	18	AAW133213	Human oestrogen re
22	2198	87.2	416	18	AAW133214	Human oestrogen re
23	2198	87.2	416	18	AAW133215	Human oestrogen re
24	2198	87.2	416	18	AAW133216	Human oestrogen re
25	2030.5	79.3	510	20	AAW04435	Human oestrogen re
26	2000.5	79.3	510	20	AAW04436	Human oestrogen re
27	1499	59.4	414	20	AAW098127	Human oestrogen re
28	1499	59.4	414	20	AAW04436	Human oestrogen re
29	1211	48.0	587	23	AAW16000	Human oestrogen re
30	1210	48.0	581	23	AAW16001	Human oestrogen re
31	1205.5	48.0	582	23	AAW16002	Human oestrogen re
32	1206	47.8	595	22	AAW084509	Human oestrogen re
33	1204	47.7	595	22	AAW21626	Human oestrogen re
34	1204	47.7	595	22	AAW084505	Human oestrogen re
35	1204	47.7	595	22	AAW084506	Human oestrogen re
36	1204	47.7	595	22	AAW084513	Human oestrogen re
37	1204	47.7	595	22	AAW084514	Human oestrogen re
38	1202	47.7	595	22	AAW084515	Human oestrogen re
39	1201	47.6	595	22	AAW084507	Human oestrogen re
40	1197	47.5	595	22	AAW084508	Human oestrogen re
41	1197	47.5	595	22	AAW084509	Human oestrogen re
42	1195	47.4	595	22	AAW084510	Human oestrogen re
43	1195	47.4	595	22	AAW084511	Human oestrogen re
44	1195	47.4	595	22	AAW084512	Human oestrogen re
45	1195	47.4	595	22	AAW084513	Human oestrogen re
46	1195	47.4	595	22	AAW084514	Human oestrogen re
47	1195	47.4	595	22	AAW084515	Human oestrogen re
48	1195	47.4	595	22	AAW084516	Human oestrogen re
49	1195	47.4	595	22	AAW084517	Human oestrogen re
50	1187	47.1	595	22	AAW084518	Human oestrogen re
51	1186.5	47.0	595	22	AAW084519	Human oestrogen re
52	1181	46.8	595	22	AAW084520	Human oestrogen re
53	1181	46.8	595	22	AAW084521	Human oestrogen re
54	1181	46.8	595	22	AAW084522	Human oestrogen re
55	1181	46.8	595	22	AAW084523	Human oestrogen re
56	1181	46.8	595	22	AAW084524	Human oestrogen re
57	1176	46.3	595	22	AAW084525	Human oestrogen re
58	1176	46.3	595	22	AAW084526	Human oestrogen re
59	1167	46.3	595	22	AAW084527	Human oestrogen re
60	1167	46.3	595	22	AAW084528	Human oestrogen re
61	1167	46.3	595	22	AAW084529	Human oestrogen re
62	1167	46.3	595	22	AAW084530	Human oestrogen re
63	1167	46.3	595	22	AAW084531	Human oestrogen re
64	1167	46.3	595	22	AAW084532	Human oestrogen re
65	1167	46.3	595	22	AAW084533	Human oestrogen re
66	1167	46.3	595	22	AAW084534	Human oestrogen re
67	1167	46.3	595	22	AAW084535	Human oestrogen re
68	1167	46.3	595	22	AAW084536	Human oestrogen re
69	1167	46.3	595	22	AAW084537	Human oestrogen re
70	1167	46.3	595	22	AAW084538	Human oestrogen re
71	1167	46.3	595	22	AAW084539	Human oestrogen re
72	1167	46.3	595	22	AAW084540	Human oestrogen re
73	1167	46.3	595	22	AAW084541	Human oestrogen re
74	1167	46.3	595	22	AAW084542	Human oestrogen re
75	1167	46.3	595	22	AAW084543	Human oestrogen re
76	1167	46.3	595	22	AAW084544	Human oestrogen re
77	1167	46.3	595	22	AAW084545	Human oestrogen re
78	1167	46.3	595	22	AAW084546	Human oestrogen re
79	1167	46.3	595	22	AAW084547	Human oestrogen re
80	1167	46.3	595	22	AAW084548	Human oestrogen re
81	1167	46.3	595	22	AAW084549	Human oestrogen re
82	1167	46.3	595	22	AAW084550	Human oestrogen re
83	1167	46.3	595	22	AAW084551	Human oestrogen re
84	1167	46.3	595	22	AAW084552	Human oestrogen re
85	1167	46.3	595	22	AAW084553	Human oestrogen re
86	1167	46.3	595	22	AAW084554	Human oestrogen re
87	1167	46.3	595	22	AAW084555	Human oestrogen re
88	1167	46.3	595	22	AAW084556	Human oestrogen re
89	1167	46.3	595	22	AAW084557	Human oestrogen re
90	1167	46.3	595	22	AAW084558	Human oestrogen re
91	1167	46.3	595	22	AAW084559	Human oestrogen re
92	1167	46.3	595	22	AAW084560	Human oestrogen re
93	1167	46.3	595	22	AAW084561	Human oestrogen re
94	1167	46.3	595	22	AAW084562	Human oestrogen re
95	1167	46.3	595	22	AAW084563	Human oestrogen re
96	1167	46.3	595	22	AAW084564	Human oestrogen re
97	1167	46.3	595	22	AAW084565	Human oestrogen re
98	1167	46.3	595	22	AAW084566	Human oestrogen re
99	1167	46.3	595	22	AAW084567	Human oestrogen re
100	1167	46.3	595	22	AAW084568	Human oestrogen re

84	64.4	25.5	4.58	2.1	AAV83482.5
85	64.4	25.5	5.08	2.1	AAV94463.7
86	64.4	25.1	4.43	2.1	AAH12970.0
87	64.0	25.0	4.43	3.9	AAV80939.1
88	64.0	25.0	4.43	2.1	AAH09966.6
89	64.0	25.0	5.00	2.1	AAV038346.0
90	64.0	25.0	5.00	2.1	AAV83832.2
91	59.8	24.7	4.74	2.2	AAU029986.0
92	59.8	24.7	4.82	2.2	AAU029558.0
93	59.7	24.7	4.86	2.4	AAH05347.7
94	59.7	24.7	5.52	2.2	AAH30411.1
95	59.4	24.6	5.21	9	AAV80939.0
96	58.4	24.1	5.56	2.2	AAV11197.7
97	57.2	22.7	4.18	2.1	AAV8382.4
98	57.0	22.6	4.18	2.0	AAV038348.0
99	52.2	20.7	4.84	2.2	AAH64255.1
100	50.4	20.0	9.9	2.2	AAV3717.3
101	46.0	18.4	5.25	2.0	AAV21625.5
102	45.8	18.2	5.4	1.4	AAH39408.8
103	45.8	18.2	5.43	1.6	AAV72483.3
104	45.8	18.2	5.43	2.3	AAU78297.7
105	45.5	18.1	4.46	1.2	AAH11837.1
106	45.5	18.1	4.46	1.5	AAH72484.4
107	45.4	18.0	5.18	1.4	AAH39465.9
108	45.4	18.0	4.10	1.4	AAH39465.9
109	44.8	17.8	9.43	2.0	AAV21621.1
110	44.8	17.8	9.43	2.1	AAV97297.7
111	44.4	17.6	4.64	1.2	AAH13800.0
112	44.4	17.6	4.64	1.4	AAH39471.1
113	44.0	17.5	4.18	1.2	AAH1222.3
114	44.0	17.4	4.64	2.4	AAU78298.7
115	43.9	17.4	3.99	2.3	AAH68238.8
116	43.7	17.3	4.52	2.0	AAV21627.7
117	43.7	17.3	4.18	2.0	AAV31493.1
118	43.7	17.3	9.19	1.0	AAV93109.9
119	43.7	17.3	9.19	1.0	AAV90996.6
120	43.7	17.3	9.19	1.8	AAW14784.4

ALUMINUM

XX	AAH4212	Standard, Protein; 477 AA.
XX	AAH4212:	
XX	20 APR 1998	(first entry)
XX	Human oestrogen receptor protein.	
XX	oestrogen receptor protein; steroid; alternative splicing; estradiol;	
KW	estrogen estiol; screening.	
XX	Homo sapiens.	
OS		
XX	E0798178-AZ.	
PB	01 OCT 1997.	
XX	25 MAR 1997;	97EP-0200903.
XX	22 NOV 1996;	96EP-0204204.
PR	26 MAR 1996;	96EP-0205820.
XX	(AIKU) AKZO NOBEL NV.	
FA	D.) Koma R., Moselman S;	
XX	WPt.: 1997/474180/A4.	
FR	N FSOBJ: PAT88412.	
XX		

Query Match	100.0%	Score 2522	DB 18	Length 477
Mat. local similarity	100.0%	Ident. No. 2	Ident. 477	
Matches 477	Conservative 0	Mismatches 0	Indels 0	Gaps 0
01	MNSYSPNSVNTNLEGGSGPQSTSPNVLWMTQDHSLSPIVNVKLSLSHAAPFQSKHWCFAEPL	60		
02				
03				
04				
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25-MAR-1996: 96EP-0200820.
 22-NOV-1996: 96EP-0203284.
 25-MAR-1997: 97EP-0200903.
 (AKU) AKZO NOBEL NV.
 Mosselman S, Dijkema K;
 WP1: 2002-084414/12.
 N-PSDB: AA172128.
 New isolated chimeric receptor comprising a DNA binding domain and/or
 ligand binding domain of a new estrogen receptor, for identifying
 functional ligands or hormonal analogs for the receptor.

Example A: Page 15-17; 35pp; English.

This sequence shows a novel estrogen receptor (ER). The gene encoding
 this new ER is located on chromosome 14 and has a different tissue
 distribution from classical ER. This ER also has two orphan ER's,
 ER-alpha and ER-beta. These orphan receptors have estrogen receptor-
 related structure but do not appear to be able to bind estradiol or other
 ER ligands. The DNA binding domain (DBD) and ligand binding domain (LBD)
 from this ER may be used in the chimeric receptor of the invention,
 which also has an N-terminal domain. The chimeric receptor, or DNA
 encoding it, is useful in a screening assay for identification of new
 drugs. Similar chimeric receptors comprising the LBD of the new ER,
 and also comprising the DBD and an N-terminal domain derived from
 another nuclear receptor e.g., progesterone receptor, are useful for the
 screening of compounds to identify new ligands or hormone analogs which
 are able to activate the new ER. Chimeric receptors comprising a DBD
 of the new ER, and LBD and an N-terminal domain derived from
 another nuclear receptor, can be used to identify new ligands or
 hormone analogs for the nuclear receptors.

Sequence 477 AA:

Query Match: 100.0%; Score 2522; DB 23; Length 477;
 Best Local Similarity: 100.0%; Pred. No. 2; Le-231;
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNYSIPSNVTNLEGGPGRRPTSPNVLPPTGHLSPVVRHQLSHLYAEFGKSWCFARSL 60
 1 MNYSIPSNVTNLEGGPGRRPTSPNVLPPTGHLSPVVRHQLSHLYAEFGKSWCFARSL 60
 61 EHTLPVNRPTLKRKVSNGRCASPVTPGSKRDHAFCAVCSGVASGYHYGWSCEGKAF 120
 61 EHTLPVNRPTLKRKVSNGRCASPVTPGSKRDHAFCAVCSGVASGYHYGWSCEGKAF 120
 61 EHTLPVNRPTLKRKVSNGRCASPVTPGSKRDHAFCAVCSGVASGYHYGWSCEGKAF 120
 121 KRSTGHNHYTGPATNWTIKNPKKSGQACPIKCYEVGMVCGSPREPGYRIYLRQR 180
 121 KRSTGHNHYTGPATNWTIKNPKKSGQACPIKCYEVGMVCGSPREPGYRIYLRQR 180
 121 KRSTGHNHYTGPATNWTIKNPKKSGQACPIKCYEVGMVCGSPREPGYRIYLRQR 180
 181 SADRQIHCAGAKKSGHAPVRRLDIALSPQIVITLLEAPRVILISRPAPTEAS 240
 181 SADRQIHCAGAKKSGHAPVRRLDIALSPQIVITLLEAPRVILISRPAPTEAS 240
 181 SADRQIHCAGAKKSGHAPVRRLDIALSPQIVITLLEAPRVILISRPAPTEAS 240
 241 MNMSITKLADKELVHMSMAKRIQGEVELSLFDVRLLESCGMEVIMMLIMKSLDHPK 300
 241 MNMSITKLADKELVHMSMAKRIQGEVELSLFDVRLLESCGMEVIMMLIMKSLDHPK 300
 241 MNMSITKLADKELVHMSMAKRIQGEVELSLFDVRLLESCGMEVIMMLIMKSLDHPK 300
 301 LIFAPDVLVDKDEKCVHGILIEFDMLATTISPRRELKIOHKREYLVKAMILLNSSMYPL 360
 301 LIFAPDVLVDKDEKCVHGILIEFDMLATTISPRRELKIOHKREYLVKAMILLNSSMYPL 360
 301 LIFAPDVLVDKDEKCVHGILIEFDMLATTISPRRELKIOHKREYLVKAMILLNSSMYPL 360
 361 VTATQDAPSSKRLHLNAVTDALVWVIAKSGISSQDSMRLANILMLSHVHANSKKG 420
 361 VTATQDAPSSKRLHLNAVTDALVWVIAKSGISSQDSMRLANILMLSHVHANSKKG 420
 361 VTATQDAPSSKRLHLNAVTDALVWVIAKSGISSQDSMRLANILMLSHVHANSKKG 420
 421 EHLNMGKRNVPVYFLLTFLMNAHVLGCKSSITFSEGSPADESKSGESQNDQSG 477
 421 EHLNMGKRNVPVYFLLTFLMNAHVLGCKSSITFSEGSPADESKSGESQNDQSG 477
 421 EHLNMGKRNVPVYFLLTFLMNAHVLGCKSSITFSEGSPADESKSGESQNDQSG 477

RESULT 3
 AAW33215
 10 AAW33215 standard: Protein: 530 AA.

AAW33215:

20 APR-1998 (first entry)

Human oestrogen receptor protein #2.

Oestrogen receptor protein; steroid; alternative splicing; estradiol;
 estone; estrogen; screening.

Homo sapiens.

EP798478-A2.

01-OCT-1997.

25-MAR-1997: 97EP-0200903.

22-NOV-1996: 96EP-0203284.

25-MAR-1996: 96EP-0200820.

(AKU) AKZO NOBEL NV.

Dijkema K, Mosselman S;

WP1: 1997-473188/44.

N-PSDB: AA188415.

DNA encoding estrogen receptor useful in screening assay to
 identify novel ligands or hormonal analogues

Claim 4: Page 35-37; 45pp; English.

This sequence represents a novel estrogen binding protein isolated from
 human testis cDNA in order to study upstream translation initiation
 proteins using 5' RACE-PCR technology. This receptor is able to bind and
 be activated by estradiol, estone and estrilol, can be used in a screening
 assay for the identification of new drugs e.g. novel ligands or hormonal
 analogues.

Sequence 530 AA:

Query Match: 100.0%; Score 2522; DB 18; Length 530;
 Best Local Similarity: 100.0%; Pred. No. 2; Le-241;
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNYSIPSNVTNLEGGPGRRPTSPNVLPPTGHLSPVVRHQLSHLYAEFGKSWCFARSL 60
 1 MNYSIPSNVTNLEGGPGRRPTSPNVLPPTGHLSPVVRHQLSHLYAEFGKSWCFARSL 60
 54 MNYSIPSNVTNLEGGPGRRPTSPNVLPPTGHLSPVVRHQLSHLYAEFGKSWCFARSL 113
 61 EHTLPVNRPTLKRKVSNGRCASPVTPGSKRDHAFCAVCSGVASGYHYGWSCEGKAF 120
 61 EHTLPVNRPTLKRKVSNGRCASPVTPGSKRDHAFCAVCSGVASGYHYGWSCEGKAF 120
 114 EHTLPVNRPTLKRKVSNGRCASPVTPGSKRDHAFCAVCSGVASGYHYGWSCEGKAF 173
 121 KRSTGHNHYTGPATNWTIKNPKKSGQACPIKCYEVGMVCGSPREPGYRIYLRQR 180
 121 KRSTGHNHYTGPATNWTIKNPKKSGQACPIKCYEVGMVCGSPREPGYRIYLRQR 180
 174 KRSTGHNHYTGPATNWTIKNPKKSGQACPIKCYEVGMVCGSPREPGYRIYLRQR 233
 181 SADRQIHCAGAKKSGHAPVRRLDIALSPQIVITLLEAPRVILISRPAPTEAS 240
 181 SADRQIHCAGAKKSGHAPVRRLDIALSPQIVITLLEAPRVILISRPAPTEAS 240
 234 SADRQIHCAGAKKSGHAPVRRLDIALSPQIVITLLEAPRVILISRPAPTEAS 293
 241 MNMSITKLADKELVHMSMAKRIQGEVELSLFDVRLLESCGMEVIMMLIMKSLDHPK 300
 241 MNMSITKLADKELVHMSMAKRIQGEVELSLFDVRLLESCGMEVIMMLIMKSLDHPK 300
 241 MNMSITKLADKELVHMSMAKRIQGEVELSLFDVRLLESCGMEVIMMLIMKSLDHPK 300
 301 LIFAPDVLVDKDEKCVHGILIEFDMLATTISPRRELKIOHKREYLVKAMILLNSSMYPL 360
 301 LIFAPDVLVDKDEKCVHGILIEFDMLATTISPRRELKIOHKREYLVKAMILLNSSMYPL 360
 361 VTATQDAPSSKRLHLNAVTDALVWVIAKSGISSQDSMRLANILMLSHVHANSKKG 420
 361 VTATQDAPSSKRLHLNAVTDALVWVIAKSGISSQDSMRLANILMLSHVHANSKKG 420
 421 EHLNMGKRNVPVYFLLTFLMNAHVLGCKSSITFSEGSPADESKSGESQNDQSG 477
 421 EHLNMGKRNVPVYFLLTFLMNAHVLGCKSSITFSEGSPADESKSGESQNDQSG 477
 421 EHLNMGKRNVPVYFLLTFLMNAHVLGCKSSITFSEGSPADESKSGESQNDQSG 477


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UY 401 VTATVDALSSSRKLAHLNAVTDALVWVAKSGISSGQOOSMRANLMLSHVHASNKR 420
IB 414 VTATVDALSSSRKLAHLNAVTDALVWVAKSGISSGQOOSMRANLMLSHVHASNKR 474
UY 421 EHLINMKGNVVPYVDLLEMLNAHVLRGKSSITGSESPASRKSRSQNPQSQ 477
IB 474 EHLINMKGNVVPYVDLLEMLNAHVLRGKSSITGSESPASRKSRSQNPQSQ 540

RESULT 4
AAW07858
IB AAW07858 standard; Protein: 540 AA.
XX
XX AAW07858;
XX
XX 07 JUN 1999 (first entry)
XX
XX Human oestrogen receptor-beta.
XX
XX oestrogen receptor-beta: hkr-beta: human.
XX
XX Homo sapiens.
XX
XX W09907847 A1.
XX
XX 18 FEB 1999.
XX
XX 20 JUL 1998; 98WD 0514944.
XX
XX 05 AUG 1997; 97DS-0906465.
XX
XX (AMMP) AMERICAN HOME PROD CORP.
XX
XX Bhat RA, Henderson RA, Hsiao C, Karadimas SK;
XX
XX W01: 1999-167424/14.
XX
XX N-PSDB: AAX24364.
XX
XX Human oestrogen receptor beta coding sequence useful in the
XX production of human oestrogen receptor beta and identification of
XX human oestrogen receptor beta interactive compounds
XX
XX Claim 17: Page 42-44; 49pp; English.
XX
XX This polypeptide comprises a full-length human oestrogen receptor beta
XX (hkr-beta), including 45 previously unknown N-terminal amino acid
XX residues that are believed to contribute to the transcription
XX activation function of the receptor. The amino acid sequence was
XX deduced from the nucleotide sequence (see AAX24364) of an isolated
XX cDNA clone. hkr-beta is selectively expressed in the thymus,
XX spleen, ovary and testes. The invention encompasses hkr-beta
XX polypeptides and polypeptides, particularly peptides which
XX include residues 1-45 of hkr-beta. The invention also provides
XX expression systems in which transcriptionally active hkr-beta or
XX fragments can be produced, as well as screening methods for
XX identifying hkr-beta agonists and antagonists (including
XX tissue specific oestrogens and anti-oestrogens), and hkr-beta
XX co-activators and inhibitors.
XX
XX Sequence: 540 AA;
XX
XX Query Match: 100.0%; Score: 25.22; ID: 20; Length: 540;
XX best local similarity: 100.0%; Prod. No. 2; 50 231;
XX Matches: 477; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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UY 121 KRSLGGNDYLCPPALNCTLRKNPKSVQAQLKCYEVMVKGVSRRRCYELVROR 180
IB 174 KRSLGGNDYLCPPALNCTLRKNPKSVQAQLKCYEVMVKGVSRRRCYELVROR 234
UY 181 SADDPLDVCACAKKSGCHAVRPRLLDAASPTQLVLTLLAPPPVLTSGKAPPTAS 240
IB 244 SADDPLDVCACAKKSGCHAVRPRLLDAASPTQLVLTLLAPPPVLTSGKAPPTAS 294
UY 241 MMSSTLKALOKELVHMLSMNKLPGVEELSPQVRLTESQWELMMLMMSIDHKK 300
IB 294 MMSSTLKALOKELVHMLSMNKLPGVEELSPQVRLTESQWELMMLMMSIDHKK 354
UY 401 LIFAPDVLDRDREGKVGSLLEFDMLLATISPRRLKIQHKEYLVKAMILLNSMYPL 460
IB 454 LIFAPDVLDRDREGKVGSLLEFDMLLATISPRRLKIQHKEYLVKAMILLNSMYPL 414
UY 461 VTATVDALSSSRKLAHLNAVTDALVWVAKSGISSGQOOSMRANLMLSHVHASNKR 420
IB 414 VTATVDALSSSRKLAHLNAVTDALVWVAKSGISSGQOOSMRANLMLSHVHASNKR 474
UY 421 EHLINMKGNVVPYVDLLEMLNAHVLRGKSSITGSESPASRKSRSQNPQSQ 477
IB 474 EHLINMKGNVVPYVDLLEMLNAHVLRGKSSITGSESPASRKSRSQNPQSQ 540

RESULT 5
AAE10457
IB AAE10457 standard; Protein: 540 AA.
XX
XX AAE10457;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human estrogen receptor (ER)-beta protein.
XX
XX ER: estrogen receptor-beta; dietary compound; environmental pollutant;
XX red wine; ER-beta mediated cell growth inhibitor modulator: human.
XX
XX Homo sapiens.
XX
XX W0200169262 A1.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001W0-US08276.
XX
XX 15-MAR-2000; 2000US 189605P.
XX
XX (OYMA-) UNIV MASSACHUSETTS.
XX
XX Ho S;
XX
XX W01: 2001-596920/67.
XX
XX N-PSDB: AAD18442.
XX
XX In vitro screening for modulator of estrogen receptor-beta-mediated
XX cell growth inhibition by contacting cell having functional ER-beta
XX protein with candidate compound and detecting ER-beta-regulated gene
XX expression.
XX
XX Example 4: Fig 7A; 49pp; English.
XX
XX The invention relates to in vitro screening for modulator of estrogen
XX receptor-beta (ER-beta)-mediated cell growth inhibition. The method
XX involves contacting mammalian cell having functional ER-beta protein
XX with candidate compound and detecting increase/decrease of ER-beta
XX regulated gene expression in presence of candidate compound compared
XX to expression in absence of the compound. The method is useful for
XX identifying a compound that modulates ER-beta-mediated cell growth
XX inhibition. It is useful for testing dietary compounds, e.g., red wine,
XX for the presence of estrogen mimics that trigger ER-beta-mediated
XX processes, thus affecting physiological function positively or

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negatively and for testing environmental pollutants for the presence of estrogen mimics that may pose health risks involving ER-beta-mediated processes. The present sequence is human ER-beta protein.

Sequence 530 AA;

Query Match	100.00;	Score 2.522;	Length 510;
Host Local Similarity	100.00;	Prod. No. 2.50e231;	
Matches 477; Conservative	0;	Mismatches	0;
		Indels	0;
		Gaps	0;

[illegible]

REFERENCES

AAU27322
ID: AAU27322 standard; Protein, 530 AA
v

AC: AAIJ 27 3229

DT 18-KC-2001 (first entry)

Human α_1 adrenergic receptor beta.

Human breast region receptor beta, EPRbeta, SNP, chromosome 6q.25.1;

KM autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism
 KW osteoarthritis; osteoporosis; breast cancer; endometrial cancer.

Homō sapiētis.

PN W020016,2793-A2.

PLD 30-AUG-2001. 22

PH 20-FRR-2001; 2001WO-US05360.

PR 22-FRB-2000; 200005-0183755
24-TAM-2001; 200115-0768705

XX
XX
(DELETED) DE COMB NY

XX
XX
PI
Kajush E. (Jaco) M.

DR WPI, 2001 582241/65
DR N-PSDB; AAS43105, A

DR N-PSIB; AAS43105, AAS43104

PT test: estrogen receptor gene and protein polymorphisms useful for diagnosis of individuals at risk of developing bone disorders

TS Enclosure; Figure 4; 245pp; English.

The invention relates to a novel isolated peptide comprising or consisting of an amino acid sequence selected from an amino acid sequence of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of 10 amino acids), antibodies against them, nucleic acids encoding them (including vectors for transforming cells). The gene for human ERbeta is located on chromosome 6q 25.1. The variant are encoded by single nucleotide polymorphisms (SNP). The variant peptides and proteins can be used in assays to determine the biological activity of the protein, to raise antibodies, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, to identify compounds that modulate receptor activity and to screen compounds for the ability to stimulate or inhibit interaction between the receptor protein and a target molecule that normally interacts with the receptor protein e.g. oestrogen. The antibody can be used to isolate the protein, to assess expression in disease states e.g. cardiovascular disease and autoimmune disease (e.g. systemic lupus erythematosus, arthritis, rheumatism and osteoarthritis), osteoporosis, breast cancer and endometrial cancer. In addition the antibodies can be used in pharmacogenomic analysis and inhibiting protein function, e.g. blocking the binding of the oestrogen receptor protein to a binding partner such as a ligand. The nucleic acids encoding the proteins can be used as probes, primers, chemical intermediates and in biological assays. The present sequence represents human ERbeta.

sq Sequence 530 AA;

Query Match:	100.0%	Score 2522	PI 2.2	Length 530
Best local Similarity:	100.0%	Prod. No. 2.5e-231		
Matches 477; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

[illegible]

RESULT

AA660649		standard; protein; 540 AA.
1D	AA660649	
XX		
AC	AA660649:	
XX		
1E	04 MAY 2001	(first entry)
XX		
DE	Human oestrogen receptor beta (ER beta); SFQ ID No.1.	
XX		
KM	Human oestrogen receptor beta; ER-beta; labelled hormone receptor;	
KW	optical signal; ligand binding; hormonal disorder;	
KX	sex hormone associated; ovulation; drug screening; drug discovery;	
XX		
GZ	Homo sapiens.	
XX		
FN	M0200107019 AI.	
XX		
1D	01 FEB 2001.	
XX		
FE	24 JUL 2000; 2000MO JP04940.	
XX		
F8	24 JUL 1999; 99JP 0209860.	
XX	41 MAY 2000; 2000JP-0164479.	
F9	41 MAY 2000; 2000JP-0164476.	
XX		
FA	(OJYO) OLYMPUS OPTICAL CO LTD.	
XX		
F1	Sakamoto H., Kato N;	
XX		
1B	WFI: 2001 J46581/17.	
1B	N FSIHQ; AAF99897.	
XX		
F7	determination of the interaction of a substance for investigation and	
F4	diagnosis of hormonal disorders using an optically labeled receptor	
F1	protein	
XX		
PS	claim 26; page 68-72; 75pp; Japanese.	
XX		
CE	The invention relates to a method for examining the interaction of a	
CE	test substance with a hormone receptor protein. The method involves	
CE	conducting a test substance with a hormone receptor protein (e.g., an	
CE	oestrogen receptor) which is labelled with an optical marker (e.g., a	
CE	fluorescent protein), where the marker is capable of undergoing a change	
CE	in its optical properties when the receptor binds a ligand. The optical	
CE	signal generated in the presence of the test compound is then compared	
CE	with that generated in the absence of the test compound to determine	
CE	whether the test compound is interacting with the hormone receptor	
CE	protein. The invention also encompasses the labelled hormone receptor	
CE	protein, the gene encoding it, and vectors and host cells comprising	
CE	such genes. The method of the invention is used for the investigation	
CE	and diagnosis of hormonal disorders, especially those associated with	
CE	sex hormones e.g., suppression of ovulation. The present sequence	
CE	represents human oestrogen receptor beta (ER beta).	
XX		
5U	Sequence 540 AA:	
Query Match	100.0%; Score 2522; DB 22; Length 540;	
Best Local Similarity	100.0%; Proc. No. 2; Sg 241;	
Matches 477;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
UY	1 MYSTPSNVNLEGGGCGTTSFNYMLTFPGHLSPLVNHQLSHELVAPGKSHWEARSL	60
DB		
5A	MNSTPSSNTLRECHGKHQTSPNVLMTFGHSPLVNHQLSHELVAPGKSHWEARSL	114
UY	61 EHTLPVNRKTEKKRSGNWCAASPVTPGSKRPAHPVAVSIVYASGVHYVMSSEYKAPE	120
DB		
1B	EHTLPVNRKTEKKRSGNWCAASPVTPGSKRPAHPVAVSIVYASGVHYVMSSEYKAPE	174
UY	121 KRSTGGRHATCTATAGCTTTLRNKRSKSYQAHLAKTYEVAMVAASRKAECTICVLRQR	180
DB		
1B	KRSTGGRHNDYCTPATNGCTTDRNKRSKYQAHLAKRYELAVMAVGGRRETCYELVRGR	234
UY	181 SAADGLDFANAKKRSKGAAPVVRLDVALASTIQLVTLLDAEPRIIVLTSPDSAPETFS	240

PA (M:R I) M:RCK & CO INC

Acquorea victoria

05	Homo sapiens
XX	
UN	W200240694 AL
XX	
FD	210 30N 2002
XX	
FE	14 DEC 2001, 2001W0 JH099B,
XX	
FE	14 DEC 2000; 2000JJP-080027,
XX	
FE	10 JAN 2001; 2001JF 9022105,
XX	
FA	(CLYU) OLYMPOS OPTICAL, CO LTD,
XX	
FI	Kato N, Sakamoto H;
XX	
DK	W01; 2002 5,28176/56,
DK	N P50B; A8N6125,
XX	
XX	
FE	Autorefractive function-embedded contact optics-based fluorometric
FE	analyzers for studying behaviors of fluorescent labeled molecules
FE	particularly intracellular biological molecules like proteins at
FE	molecular level

Example 2: Page 98-105; 109pp; Japanese.

106	677	VATGVNDSKRLAHLLNAVDAIYVWYIAKSTISDQDSIMLAMLISVYKASKCKM	786
Q7	421	EHLLNKKRKVVVYVYVLLLEMLNAVYDQKSSSLTSTSTSVAFESKSKSTFSGNIGSQ	477
107	151	EHLLNKKRKVVVYVYVLLLEMLNAVYDQKSSSLTSTSTSVAFESKSKSTFSGNIGSQ	793

RESULT 11
AAW14724 Standard: Protoclin; 485 AA.

XX	ADAM14/24	
XX	08-JUN-1997 (first entry)	
DT		
XX		
XX	Human oestrogen receptor beta (ER-beta) :	
DE		
XX		
KW	cellular receptor; oestrogen receptor beta; ER-beta;	
KW	nuclear receptor; prostate cancer; benign prostatic	
KW	hyperplasia;	
KW	cellular cancer; cardiovascular disease; osteoporosis;	
KW	environment; pollutant.	
XX		
XX	Homo sapiens.	
OS		
XX		
XX	Key	location/qualifiers
EH		
EH	Dominin	104...169
ET		/label- DNA binding_domain
ET	Dominin	260...457
ET		/label- ligand-binding_domain
XX		
XX	W07707548-A2	
XX		

XX	09-SEP-1996;	96MD-EP04933
XX		
XX	08-MAY-1996;	96GB-0009576.
PR	08-SEP-1995;	95GB-0018272.
PR	15-MAR-1996;	96GB-0005550.
PR	11-APR-1996;	96GB-0007532.
XX		
XX	(KAKO) KAKO HIO AM.	
XX		
XX	Emmarik E., Gustafsson J., Kuiper GGJ.	
XX	WP1: 1997-192842/17.	
PR	N EPOB: AAT62843.	
XX		
XX	New isolated oestrogen receptor beta - used to develop probes for	
PI	treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular	
PI	disease	
XX		
XX	Claim 1: Fig 1A; 45pp; English.	
PS		
XX		
XX	A novel human orphan receptor (AAW14724) is related to the known	
XX	oestrogen receptor ER-alpha, and has been designated ER-beta.	
XX	It is an oestrogen receptor-related nuclear receptor. The ER-beta	
XX	amino acid sequence was deduced from a cDNA clone (AA762843) isolated	
XX	from a human testis cDNA library. Rat, human and mouse ER-beta	
XX	(AAW17243-25) can be used to isolate molecules for use in the	
XX	treatment of cardiovascular diseases, central nervous system	
XX	diseases, osteoporosis, prostate or ovarian cancer or benign	
XX	prostatic hyperplasia and to test environmental chemicals for	
XX	oestrogenic activity.	

	Query Match	Score	DB	Length
Post Local Similarity	99.68%	251.2	108.18	4855
Matched	47%	0	Mismatch	1
			Indels	0
			Gaps	0


```

Db      9  MNVSTPSNVINLEKQPGQTTSPNVLMPTFHLSPLVVRKQLSHLYAEHOKSPWCEASTL 68
QY      61  EHTLPVNPETLKRVSNMPASPVTPGSGKPAHFAVGSIDVASCYHWCVMSCEQYKAF 120
Db      69  EHTLPVNPETLKRVSNMPASPVTPGSGKPAHFAVGSIDVASCYHWCVMSCEQYKAF 128
QY      121 KRSIQCHNDYICPATNCTIDKNRPSQACPLRYEYGMKCGSRREKCYRLVRQR 180
Db      129 KRSIQCHNDYICPATNCTIDKNRPSQACPLRYEYGMKCGSRREKCYRLVRQR 188
QY      181 SAEQHLGACAKRSGSHAPRVRELLIDALSPQVLTLLEAPPPVLLISPSAPPTAS 240
Db      189 SAEQHLGACAKRSGSHAPRVRELLIDALSPQVLTLTLLEAPPPVLLISPSAPPTAS 248
QY      241 MMSLSTKLAKELVHMSAKKIPGVELSLFQVHLFSYVMEVIMMGLMPSIDHQR 400
Db      249 MMSLSTKLAKELVHMSAKKIPGVELSLFQVHLFSYVMEVIMMGLMPSIDHQR 408
QY      301 LIFAPDLVLDRECKVEGILFLPMLATTSFPRELKQHEYLGVKAMILLNSMPYL 460
Db      309 LIFAPDLVLDRECKVEGILFLPMLATTSFPRELKQHEYLGVKAMILLNSMPYL 468
QY      361 VTATQADSSSKLAHLINAVTDALVWYIAKSGISSQGSMLANLMLLSHVRHNSKGM 420
Db      369 VTATQADSSSKLAHLINAVTDALVWYIAKSGISSQGSMLANLMLLSHVRHNSKGM 428
QY      421 EHLNMCKNVVVPYDILLEMLNAHVLPGKSSITGSESPADESKSKESUNPQSO 477
Db      429 EHLNMCKNVVVPYDILLEMLNAHVLPGKSSITGSESPADESKSKESUNPQSO 485

```

RESULT 12

AAV01597
ID AAV01597 standard; protein: 485 AA.

AC AAV01597:
D1 17-JUN-1999 (first entry)

DE An oestrogen receptor-beta protein.

KW differential oestrogen receptor; ER-alpha; ER-beta; activation;
KW Apl site; therapy.

OS Homo sapiens.

PN W09911760-A1

FD 11-MAR-1999.

FE 31-AUG-1998; 98W-0515930.

PK 04-FEB-1997; 97US-0923708.

XX (REGC) UNIV CALIFORNIA

PA Gustafsson J, Kuiper GJM, Kushner PJ, Nilsson S;

P1 Pasch K, Scandian TS, Webb P;

XX WP1: 1999-205173/17.

DB N-PSDB; AAX2686.

PT Screening for test compounds which inhibit or activate estrogen

PI receptor beta (ER-beta) mediated activation at a Apl site - for use

XX in therapy.

PS Claim 14; Page 43-44; 61pp; English.

CC The present sequence represents an estrogen receptor-beta. The

CC Specification describes a method for screening test compounds for

CC differential oestrogen receptor (ER) alpha-mediated and ER beta-mediated

CC activation at an Apl site. The method is used for identifying compounds

XX Sequence 485 AA:
SO Query Match:
98-98; Score 2493; DB 20; Length 485;
Ident Local Similarity 99.24; Pred. No. 1,30-228;
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      1  MRSITPSNVINLEKQPGQTTSPNVLMPTFHLSPLVVRKQLSHLYAEHOKSPWCEASTL 60
Db      9  MNVSTPSNVINLEKQPGQTTSPNVLMPTFHLSPLVVRKQLSHLYAEHOKSPWCEASTL 68
QY      61  EHTLPVNPETLKRVSNMPASPVTPGSGKPAHFAVGSIDVASCYHWCVMSCEQYKAF 120
Db      69  EHTLPVNPETLKRVSNMPASPVTPGSGKPAHFAVGSIDVASCYHWCVMSCEQYKAF 128
QY      121 KRSIQCHNDYICPATNCTIDKNRPSQACPLRYEYGMKCGSRREKCYRLVRQR 180
Db      129 KRSIQCHNDYICPATNCTIDKNRPSQACPLRYEYGMKCGSRREKCYRLVRQR 188
QY      181 SAEQHLGACAKRSGSHAPRVRELLIDALSPQVLTLLEAPPPVLLISPSAPPTAS 240
Db      189 SAEQHLGACAKRSGSHAPRVRELLIDALSPQVLTLTLLEAPPPVLLISPSAPPTAS 248
QY      241 MMSLSTKLAKELVHMSAKKIPGVELSLFQVHLFSYVMEVIMMGLMPSIDHQR 400
Db      249 MMSLSTKLAKELVHMSAKKIPGVELSLFQVHLFSYVMEVIMMGLMPSIDHQR 408
QY      301 LIFAPDLVLDRECKVEGILFLPMLATTSFPRELKQHEYLGVKAMILLNSMPYL 460
Db      309 LIFAPDLVLDRECKVEGILFLPMLATTSFPRELKQHEYLGVKAMILLNSMPYL 468
QY      361 VTATQADSSSKLAHLINAVTDALVWYIAKSGISSQGSMLANLMLLSHVRHNSKGM 420
Db      369 VTATQADSSSKLAHLINAVTDALVWYIAKSGISSQGSMLANLMLLSHVRHNSKGM 428
QY      421 EHLNMCKNVVVPYDILLEMLNAHVLPGKSSITGSESPADESKSKESUNPQSO 477
Db      429 EHLNMCKNVVVPYDILLEMLNAHVLPGKSSITGSESPADESKSKESUNPQSO 485

```

RESULT 13

AAW98125
ID AAW98125 standard; protein: 549 AA.

AC AAW98125:

DI 21-JUN-1999 (first entry)

DE Mouse oestrogen receptor beta isoform mER beta-1.

KW oestrogen receptor; ER beta 1; ER beta 2; mouse; tumour;

KW diagnosis; therapy; isoform.

OS Mus musculus

PN W09905170 A1

PD 04-FEB-1999.

FE 28-JUL-1998; 98W-0515539.

PK 30-JUL-1997; 97US-0054210.

PR 28-JUL-1997; 97US-0053869.

XX (UYVA) UNIV YALE.

PI Denton R, Praston C, Galien R, Rischio-Ridgen M;

XX WP1: 1999-14282/12.

CC Human oestrogen receptor beta-3 - useful in treating and monitoring

CC tumours

QY KRSLQGHNDYICPAINQCTIDKRRKSGVACPLKCYGVGMVKCSPEPEKCYEVRGR 180
 129 KRSLQGHNDYICPAINQCTIDKRRKSGVACPLKCYGVGMVKCSPEPEKCYEVRGR 188
 QY SADEQULHACAKRKSACAHAPVVELLDAISPEQVITLLEAPPHVILSRPSAPPTAS 240
 189 SASBOVHGLNKAKEVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 248
 QY MMSSTIKLAKELVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 300
 249 MMSSTIKLAKELVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 308
 QY LLEFAPDLVLDROELKVEGILLLEFPMILALISPERELKQHEFVYVYKAMILNSSMY 360
 409 LLEFAPDLVLDROELKVEGILLLEFPMILALISPERELKQHEFVYVYKAMILNSSMY 368
 QY VVATQADSSPKLAILNAVVDALVWVIAKSSLSISQGSMDANILMLSHVRIASNRGM 420
 469 AFSQFASPSKPTLHLLNAVVDALVWVIAKSSLSISQGSMDANILMLSHVRIASNRGM 428
 QY EHLINMKRKNNVAVYDILLFEMINAVHIGKSSITGSESPVADSKSRGSGNQSQ 477
 429 EHLINMKRKNNVAVYDILLFEMINAVHIGKSSITGSESPVADSKSRGSGNQSQ 485
 RESULT 20
 AAY0443
 ID AAY0443 standard; protein: 560 AA.
 AC AAY0443:
 DE 25 JUN 1999 (first entry)
 XX
 DE Mutine mdr beta 3 clone protein sequence.
 XX
 KW Estrogen receptor beta; estrogen receptor beta; ER beta.
 XX
 OS Mus sp.
 XX
 FN W09905171 A1.
 XX
 FO 04 FEB 1999.
 XX
 PE 28 JUL 1998: 98860 DBS15540.
 XX
 PR 30 JUL 1997: 9708-0054210.
 PR 28 JUL 1997: 9708-0054869.
 XX
 PA (UYVA) UNIV YALE.
 XX
 FJ Baron K, Chambon P, Denton K, Dupont S, Garnier J.
 XX
 WP1: 1999 142854/12.
 DE N-PSDB: AAX33482.
 XX
 PP Novel murine estrogen receptor-beta genes and splice variants
 XX useful for treating estrogen receptor-beta mediated disorders
 XX
 PS claim 9; Fig 1b-4; 89pp; English.
 XX
 CC The present sequence is the murine complete estrogen receptor beta
 CC (mbr beta) cDNA also designated mbr beta 3). The protein can be used to
 CC screen for agents that modulate or block the interaction between the
 CC ER beta c protein and phytoestrogen, stilbene or triphenylethylene
 CC antiestrogens. The antibody which binds the protein and can be used in
 CC assays to detect activation of the ER beta protein and can be used for
 CC subcellular localization of the protein. The complementary nucleic acid
 CC can be used to inhibit expression of the ER beta c nucleic acid.
 XX
 SO Sequence: 560 AA.
 Query Match: 87.7%; Score 2412; 100.0%; Length 560;

Best Local Similarity: 85.7%; Proc. No. 9-40-202;
 Matches: 418; Conserved: 22; Mismatches: 40; Indels: 18; Gaps: 1;
 QY 1 MMSSTIKLAKELVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 300
 73 MMSSTIKLAKELVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 308
 QY 61 EHLINMKRKNNVAVYDILLFEMINAVHIGKSSITGSESPVADSKSRGSGNQSQ 477
 133 EHLINMKRKNNVAVYDILLFEMINAVHIGKSSITGSESPVADSKSRGSGNQSQ 485
 QY 121 KRSLQGHNDYICPAINQCTIDKRRKSGVACPLKCYGVGMVKCSPEPEKCYEVRGR 180
 193 KRSLQGHNDYICPAINQCTIDKRRKSGVACPLKCYGVGMVKCSPEPEKCYEVRGR 188
 QY 181 SADEQULHACAKRKSACAHAPVVELLDAISPEQVITLLEAPPHVILSRPSAPPTAS 240
 253 SASBOVHGLNKAKEVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 248
 QY 241 MMSSTIKLAKELVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 300
 413 MMSSTIKLAKELVIMHSMARKKIPCEVELSLDQVLELSCWMEVLMGIMRSTIDRGR 308
 QY 429 EHLINMKRKNNVAVYDILLFEMINAVHIGKSSITGSESPVADSKSRGSGNQSQ 477
 473 EHLINMKRKNNVAVYDILLFEMINAVHIGKSSITGSESPVADSKSRGSGNQSQ 485
 QY 443 EYLQVAMILLNSSMYPLVATQADSSPKLAILNAVVDALVWVIAKSSLSISQGSMDANILMLSHVRIASNRGM 420
 493 EYLQVAMILLNSSMYPLVATQADSSPKLAILNAVVDALVWVIAKSSLSISQGSMDANILMLSHVRIASNRGM 428
 QY 403 ANILMLSHVRIASNRGMANILMLSHVRIASNRGMANILMLSHVRIASNRGMANILMLSHVRIASNRGM 420
 493 ANILMLSHVRIASNRGMANILMLSHVRIASNRGMANILMLSHVRIASNRGMANILMLSHVRIASNRGM 428
 QY 463 EUSKSRG 470
 553 EUSKSRG 560
 RESULT 21
 AAM34213
 ID AAM34213 standard; protein: 416 AA.
 AC AAM34213:
 DE 20 APR 1998 (first entry)
 XX
 DE Human estrogen receptor protein exon 8 splice variant.
 XX
 KW Estrogen receptor protein; steroid; alternative splicing; estradiol;
 XX estrogen; estradiol; screening.
 XX
 OS Homo sapiens.
 XX
 FN EF798478 A2.
 XX
 FO 01 OCT 1997.
 XX
 PE 25 MAR 1997: 97EP-0200903.
 XX
 PR 22 NOV 1996: 96EP-0203284.
 PR 26 MAR 1996: 96EP-0200820.
 XX
 PA (AIKO) AKZO NOBEL NV.
 XX
 FJ De Krom K, Mosselman SI.
 XX
 WP1: 1997-474199/44.
 DE N-PSDB: AAT68413.
 XX
 PP DNA encoding estrogen receptor useful in screening assay to
 PP identify novel ligands or hormonal analogues

AAW43214 standard; Protein: 418 AA.
 XX
 AC AAW43214:
 XX
 DE 20 APR 1998 (first entry)
 XX
 DE human oestrogen receptor protein splice variant (exon 8c).
 XX
 KW oestrogen receptor protein; steroid; alternative splicing; estradiol;
 KW oestrogen; estradiol; screening.
 XX
 OS Homo sapiens.
 XX
 FN EP798478 A2.
 XX
 PD 01 OCT 1997.
 XX
 PP 25 MAR 1997; 97EP-0200903.
 XX
 PR 22 NOV 1996; 96EP-0200284.
 PR 26 MAR 1997; 96EP-0200820.
 XX
 DA (ALKU) AKZO NOBEL NV.
 XX
 PI Dijkema R, Mosselman S;
 XX
 DE WP1: 1997 474188/44.
 DE N ISDB: AAW43214.
 XX
 PP DNA encoding oestrogen receptor: useful in screening assay to
 PP identify novel ligands or hormonal analogues
 XX
 PS claim 4: Page 30-32; 45pp; English.
 XX
 CC This sequence represents a splice variant of a novel oestrogen binding
 CC protein isolated from human thymus tissue. This protein contains an
 CC alternative exon 8 (exon 8c) of the novel oestrogen receptor represented
 CC in AAW43214. This novel receptor is able to bind and be activated by
 CC estradiol, oestron and oestrop, can be used in a screening assay for the
 CC identification of new drugs e.g. novel ligands or hormonal analogues.
 CC This variant does not contain an Af-2 region and therefore probably
 CC lacks the ability to modulate transcription of target genes in a ligand
 CC dependent fashion.
 XX
 SO Sequence 418 AA.
 Query Match: 87.2%; Score 2198; DB 18; Length 418;
 Best Local Similarity 100.0%; Prod. No. 1.4e-200;
 Matches 41%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 MNSSTSNVNTNLEGGVQGTTSNVNLPPTGHSPLVVRKQSLSHYAEFGKSPWFAASL 60
 1b 1 MNSSTSNVNTNLEGGVQGTTSNVNLPPTGHSPLVVRKQSLSHYAEFGKSPWFAASL 60
 07 61 EHTLPVNRKELKKKVSNGRCASTVTGNGSKRQAHFCAVSDVASCYHYGWSCEGCKAF 120
 1b 61 EHTLPVNRKELKKKVSNGRCASTVTGNGSKRQAHFCAVSDVASCYHYGWSCEGCKAF 120
 07 121 KRSTGCHNDYCTATNCTTDKRRKSCQAKRKCYEWGWWKSGSPREYVYPLVPG 180
 1b 121 KRSTGCHNDYCTATNCTTDKRRKSCQAKRKCYEWGWWKSGSPREYVYPLVPG 180
 07 121 KRSTGCHNDYCTATNCTTDKRRKSCQAKRKCYEWGWWKSGSPREYVYPLVPG 190
 1b 121 KRSTGCHNDYCTATNCTTDKRRKSCQAKRKCYEWGWWKSGSPREYVYPLVPG 190
 07 181 SADEPDLGAGKAKKSGCHAFVRELLDMISPEQVLTITLFAAPPVLLSKRSAPETAS 240
 1b 181 SADEPDLGAGKAKKSGCHAFVRELLDMISPEQVLTITLFAAPPVLLSKRSAPETAS 240
 07 241 MMSSTLNARKELVHMSWAKIPGEVELSLHGVNLESLWMEVLMMLMKRSIDHCK 300
 1b 241 MMSSTLNARKELVHMSWAKIPGEVELSLHGVNLESLWMEVLMMLMKRSIDHCK 300
 07 401 LITAVDLVLRDGRKVESTLEFPDLATTSPEPEKLGIREYLVKAMILLNSM 460
 1b 401 LITAVDLVLRDGRKVESTLEFPDLATTSPEPEKLGIREYLVKAMILLNSM 460

07 461 VIATGDASSRSKLAHLINAVYDAWVVAASSTSSGWSMRLANIMLSKRIA 415
 1b 461 VIATGDASSRSKLAHLINAVYDAWVVAASSTSSGWSMRLANIMLSKRIA 415
 RESULT 24
 AAW47846
 1b AAW47846 standard; Protein: 418 AA.
 XX
 AC AAW47846:
 XX
 DE 25-MAR-2002 (first entry)
 XX
 DE ER splice variant ER alpha.
 XX
 PP DNA binding domain; ER; ligand binding domain; ER; chimeric receptor;
 KW oestrogen receptor; ER; chromosome 14; ER alpha; ER-beta; exon 8; ER;
 KW estradiol; nuclear receptor; progesterone receptor; amplification; primer;
 KW polymerase chain reaction; Af-2 region; splice variant.
 XX
 OS Homo sapiens.
 XX
 FN EP1162264 A2.
 XX
 PD 12-DEC-2001.
 XX
 PP 25 MAR 1997; 2001EP-0202021.
 XX
 PR 26 MAR-1996; 96EP-0200820.
 PR 22-NV-1996; 96EP-0200284.
 PR 25-MAR-1997; 97EP-0200903.
 XX
 DA (ALKU) AKZO NOBEL NV.
 XX
 PI Mosselman S, Dijkema R;
 XX
 DE WP1: 2002 084414/12.
 DE N-PSDB: AA172146.
 XX
 PP New isolated chimeric receptor comprising a DNA binding domain and/or
 PP ligand binding domain of a new oestrogen receptor, for identifying
 PP functional ligands or hormonal analogs for the receptor
 XX
 PS Example B: Page 24-25; 45pp; English.
 XX
 CC The sequences given in AAW47836 and AAW47847 show splice variants
 CC of a novel oestrogen receptor (ER). The gene encoding this new ER is
 CC located on chromosome 14 and has a different tissue distribution from
 CC classical ER. This ER also has two orphan ER's, ER-alpha and ER-beta.
 CC These orphan receptors have oestrogen receptor related structure but do
 CC not appear to be able to bind estradiol or other ER ligands. These
 CC splice variants differ from the parent ER around exon 8. one clone
 CC contains exon 8B through alternative splicing. This causes an immediate
 CC termination of the reading thereby creating a truncated ER at the carboxy
 CC terminus. The other splice variant contains an alternative exon 8, exon
 CC 8c, which encodes two C-terminal amino acids and then has a stop codon.
 CC The splice variant proteins do not contain the Af-2 region and therefore
 CC probably lack the ability to modulate transcription of target genes in
 CC a ligand dependant manner. However they may be able to interfere with
 CC the functioning of the ER classical ER or the novel ER of the invention,
 CC either by heterodimerisation or by occupying oestrogen response elements
 CC or by interactions with other transcription factors.
 XX
 SO Sequence 418 AA;
 Query Match: 87.2%; Score 2198; DB 24; Length 418;
 Best Local Similarity 100.0%; Prod. No. 1.4e-200;
 Matches 41%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 MNSSTSNVNTNLEGGVQGTTSNVNLPPTGHSPLVVRKQSLSHYAEFGKSPWFAASL 60
 1b 1 MNSSTSNVNTNLEGGVQGTTSNVNLPPTGHSPLVVRKQSLSHYAEFGKSPWFAASL 60


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61 EHTLPVNRRLKPKKVSQNPASVVTSPKSKGAPSSAVSSTVASVYRQVWSSPPKAF 120
|||||
61 EHTLPVNRRLKPKKVSQNPASVVTSPKSKGAPSSAVSSTVASVYRQVWSSPPKAF 120
|||||
121 KRSLQHNINYTGATWCTTQKPKPSQACPIPKCYEVSQKQSSSPSPCYRVPQRP 180
|||||
121 KRSLQHNINYTGATWCTTQKPKPSQACPIPKCYEVSQKQSSSPSPCYRVPQRP 180
|||||
121 KRSLQHNINYTGATWCTTQKPKPSQACPIPKCYEVSQKQSSSPSPCYRVPQRP 180
|||||
181 SAEQVHCAKAKPSQSHAPVPELIDAI SPPQVITLLEAPPHVILSPISAPPTAS 240
|||||
181 SAEQVHCAKAKPSQSHAPVPELIDAI SPPQVITLLEAPPHVILSPISAPPTAS 240
|||||
181 SAEQVHCAKAKPSQSHAPVPELIDAI SPPQVITLLEAPPHVILSPISAPPTAS 240
|||||
241 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 300
|||||
241 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 300
|||||
241 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 300
|||||
301 LIFAPQVILDRPKQVEGILPFDMLATTSPPPELKHQKEVLCVKAMILLNSSMPTL 360
|||||
301 LIFAPQVILDRPKQVEGILPFDMLATTSPPPELKHQKEVLCVKAMILLNSSMPTL 360
|||||
301 LIFAPQVILDRPKQVEGILPFDMLATTSPPPELKHQKEVLCVKAMILLNSSMPTL 360
|||||
361 VTATQADSSRKLAHLNAVTDAI VVVIKSGISGQSSQSMRLANILLSHVRIA 415
|||||
361 VTATQADSSRKLAHLNAVTDAI VVVIKSGISGQSSQSMRLANILLSHVRIA 415
|||||
361 VTATQADSSRKLAHLNAVTDAI VVVIKSGISGQSSQSMRLANILLSHVRIA 415
|||||

RESULT 25
AAV04435 standard: Protein: 510 AA
AAV04435:
25-JUN-1999 (first entry)
MURINE mkr beta-2 clone protein sequence.
ESTROGEN RECEPTOR BETA: OESTROGEN RECEPTOR BETA: ER BETA.
Mus sp
W09905171-A1
04-FEB-1999.
28-JUL-1998: 98W0-0815540.
30-JUL-1997: 970S-0054210.
28-JUL-1997: 970S-0054869.
(DYYA ) UNIV YALE.
Barton K, Chambon P, Denton R, Dupont S, Garnier J.
W09905170-A1.
04-FEB-1999.
28-JUL-1998: 98W0-0815549.
30-JUL-1997: 970S-0054210.
28-JUL-1997: 970S-0054869.
(DYYA ) UNIV YALE.
Barton K, Fraston C, Gallien K, Kischke-Kron M.
W09905172.
28-JUL-1997: 970S-0054210.
28-JUL-1997: 970S-0054869.
(DYYA ) UNIV YALE.
The present invention describes the murine complete oestrogen receptor
beta (mkr beta c) also designated mkr beta-3). The present sequence
represents mkr beta-2, which is an isoform of mkr beta c. The protein
can be used to screen for agents that modulate or block the interaction
between the ER beta c protein and physiological, stilbene or
trihydroxyethylene (anti)estrogens. The antibody which binds the protein
can be used in assays to detect activation of the ER beta protein and
complementary nucleic acid can be used to inhibit expression of the
ER beta c nucleic acid.
Sequence 510 AA:

```

```

Query Match: 2438 Score 2000.50. Db:
Seq: Loc: 1. Similarity: 99.78%. Pred: R0.1.2e-181.
Matches: 465. Conservative: 222. Mismatches: 31. Gaps: 1.

QY 1 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 400
DB 74 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 400
QY 61 EHTLPVNRRLKPKKVSQNPASVVTSPKSKGAPSSAVSSTVASVYRQVWSSPPKAF 120
DB 74 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 400
QY 181 SAEQVHCAKAKPSQSHAPVPELIDAI SPPQVITLLEAPPHVILSPISAPPTAS 240
DB 143 EHTLPVNRRLKPKKVSQNPASVVTSPKSKGAPSSAVSSTVASVYRQVWSSPPKAF 192
QY 121 KRSLQHNINYTGATWCTTQKPKPSQACPIPKCYEVSQKQSSSPSPCYRVPQRP 180
DB 193 KRSLQHNINYTGATWCTTQKPKPSQACPIPKCYEVSQKQSSSPSPCYRVPQRP 180
QY 181 SAEQVHCAKAKPSQSHAPVPELIDAI SPPQVITLLEAPPHVILSPISAPPTAS 240
DB 214 SAEQVHCAKAKPSQSHAPVPELIDAI SPPQVITLLEAPPHVILSPISAPPTAS 240
QY 241 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 300
DB 274 MMSSTIKLAKRELVHMSAKKIPGFVELSLFDQVRLLESCWMEVLMGLMWSIDHCK 333
QY 301 LIFAPQVILDRPKQVEGILPFDMLATTSPPPELKHQKEVLCVKAMILLNSSMPTL 360
DB 334 LIFAPQVILDRPKQVEGILPFDMLATTSPPPELKHQKEVLCVKAMILLNSSMPTL 393
QY 361 VTATQADSSRKLAHLNAVTDAI VVVIKSGISGQSSQSMRLANILLSHVRIA 420
DB 394 ATAGQFAESSPKLTHLNAVTDAI VVVIKSGISGQSSQSMRLANILLSHVRIA 453
QY 421 EHTLPVNRRLKPKKVSQNPASVVTSPKSKGAPSSAVSSTVASVYRQVWSSPPKAF 477
DB 454 EHTLPVNRRLKPKKVSQNPASVVTSPKSKGAPSSAVSSTVASVYRQVWSSPPKAF 510

RESULT 26
AAW98126 standard: Protein: 510 AA.
AAW98126:
21-JUN-1999 (first entry)
MOUSE oestrogen receptor beta isoform mkr beta-2.
OESTROGEN RECEPTOR: ER BETA-2: ER BETA (c) MOUSE: TUMOUR.
diagnosis: therapy: isoform.
Mus musculus.
W09905170-A1.
04-FEB-1999.
28-JUL-1998: 98W0-0815549.
30-JUL-1997: 970S-0054210.
28-JUL-1997: 970S-0054869.
(DYYA ) UNIV YALE.
Barton K, Fraston C, Gallien K, Kischke-Kron M.
W09905172.
28-JUL-1997: 970S-0054210.
28-JUL-1997: 970S-0054869.
(DYYA ) UNIV YALE.
The present sequence is alternatively spliced isoform mkr beta 2
Example 2: Fig 2b: English.

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AC AAY04446:
 XX 25 JUN-1999 (first entry)
 XX Rat ER beta-4 clone protein sequence.
 XX
 XX Estrogen receptor beta: estrogen receptor beta: ER beta.
 XX
 XX Rattus sp.
 XX W09905171-A1.
 XX
 XX 04-FEB-1999.
 XX
 XX 28-JUL-1998: 98W0-0515540.
 XX
 XX 30-JUL-1997: 9708-0054210.
 XX 28-JUL-1997: 9708-0053859.
 XX
 XX (UYYA) UNIV YALE.
 XX
 XX Baron R, Chambon P, Beonten R, Dupont S, Garnier J;
 XX WPL: 1999-14285/12.
 XX
 XX Claim 9: Fig 2c: 8ypp: English.
 XX
 XX The present invention describes the murine complete estrogen receptor
 XX beta (mER beta c), also designated mER beta-3). The present sequence
 XX represents the rat isoform ER beta-4 of mER beta c. The protein can
 XX be used to screen for agents that modulate or block the interaction
 XX between the ER beta c protein and physiological, stillborn or
 XX triphenylene (anti)estrogens. The antibody which binds the protein
 XX can be used in assays to detect activation of the ER beta protein and
 XX can be used for subcellular localization of the protein. The
 XX complementary nucleic acid can be used to inhibit expression of the
 XX ER beta c nucleic acid.
 XX
 XX Sequence 730 AA:
 XX
 XX Query Match 59.4%; Score 1499; DB 20; Length 730;
 XX Best Local Similarity 87.8%; Pred. No. 1,26-133;
 XX Matches 273; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
 XX
 XX 1 MNYSPSNVNLGGGRGRTSPNVLPFTGHLSPVVRHQLSHYAEFGKSTWCEARSL 60
 XX 73 MNYSPVSGISNLDGCPRLSTSPNVLPFTGHLSPVVRHQLSHYAEFGKSTWCEARSL 132
 XX 61 EHTLPVNRFTLKRKVSNGPCASPVTPGSKRDHAFCAVCSGVHGVWVSFGCKAF 120
 XX 133 EHTLPVNRFTLKRKVSNGPCASPVTPGSKRDHAFCAVCSGVHGVWVSFGCKAF 192
 XX 121 KRSLGCHNDYTGATNCTTTPKRPKSKQACPI KCYFVGMVKGCSRPFGCYPLVRKQ 180
 XX 193 KRSLGCHNDYTGATNCTTTPKRPKSKQACPI KCYFVGMVKGCSRPFGCYPLVRKQ 252
 XX 181 SADIOLHGCARAKSCGHAPVPELIDALSPDLVITLLEAPRHVLLSRPAPFTAS 240
 XX 253 SSSSGVHGLSKAKNGCHAPVPELIDALSPDLVITLLEAPRHVLLSRPAPFTAS 412
 XX 241 MMSSTKRLAKPIVHMTSMARK PPEVEI SLFVWLLFSQWMEVIMMLMWSFHHK 400
 XX 413 MMSSTKRLAKPIVHMTSMARK PPEVEI SLFVWLLFSQWMEVIMMLMWSFHHK 472
 XX 401 LIFAPDLVDLR 311
 XX 473 LIFAPDLVDLR 383
 XX
 XX RESULT 29

AAB81600
 ID AAB81600 standard; Protein: 587 AA.
 AC AAB81600:
 XX 19-SEP-2002 (first entry)
 XX
 XX Calman crocodilus estrogen receptor protein Sku ID No:1.
 XX
 XX Calman crocodilus; estrogen receptor; endocrine disrupter; receptor.
 XX
 XX Calman crocodilus.
 XX W0200248160-A1.
 XX
 XX 20-JUN-2002.
 XX
 XX 15-NOV-2001: 2001W0-J09996.
 XX
 XX 14-DEC-2000: 2000JP-0379994.
 XX
 XX (SOMO) SOMIYOMO CHEM CO LTD.
 XX
 XX Sumida K;
 XX WPL: 2002-557614/59.
 XX N-PSDB; A0072931.
 XX
 XX The present sequence represents an estrogen receptor isolated from
 XX Calman crocodilus. The estrogen receptor gene can be used in testing
 XX systems for evaluating the ability of chemicals to control the
 XX estrogen receptor activity, e.g. assay safety of chemicals and
 XX detecting endocrine disrupters in environment and the genes and the
 XX DNA are useful in two-hybrid assays.
 XX
 XX Sequence 587 AA:
 XX
 XX Query Match 48.0%; Score 1211; DB 23; Length 587;
 XX Best Local Similarity 55.0%; Pred. No. 2,56-106;
 XX Matches 246; Conservative 71; Mismatches 106; Indels 24; Gaps 8;
 XX
 XX 22 SPNVLPFTGHLSPVVRHQLSHYAEFGKSPW--CEAFSLHTLPVNRFTLKRKVS 78
 XX 100 SPNVLPFTGHLSPVVRHQLSHYAEFGKSPW--CEAFSLHTLPVNRFTLKRKVS 156
 XX 79 RCASPVTPG-----SKRDHAFCAVCSGVHGVWVSFGCKAFKSTWCEARSL 133
 XX 157 EEMSSISKASLSMSTLKLRYCAVCSGVHGVWVSFGCKAFKSTWCEARSL 216
 XX 134 ATNCTTTPKRPKSKQACPI KCYFVGMVKGCSRPFGCYPLVRKQ 193
 XX 217 ATNCTTTPKRPKSKQACPI KCYFVGMVKGCSRPFGCYPLVRKQ 276
 XX 194 PSCHAPV-----ALSPDLVITLLEAPRHVLLSRPAPFTAS 241
 XX 277 TAEMKTPVTPGHLSPVVRHQLSHYAEFGKSPW--CEAFSLHTLPVNRFTLKRKVS 336
 XX 242 MMSSTKRLAKPIVHMTSMARK PPEVEI SLFVWLLFSQWMEVIMMLMWSFHHK 401
 XX 437 MTLTINLADKELVIMIMAKRVKPVTLTHVWHLLEFAMLTILMGLVMSKMRHPT 496
 XX 402 LFAPIVI DPEVNGVETIETPMI ATTSEPEPI KJGKEVI VYKAMILLNSMYPV 461
 XX 497 LEAVNLIDPVGKGVGVWVETIDML ATAPFPMMLDGFPEVITKSTILLNSGYTL 456
 XX 362 TATQADDSRKLALILNAVTDALVWYIAKSLISSGGSRLANLMLSHVHASKRM 420


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QY 10 INLEGGPGRO-----ITSPVIMPTGHSPLIVVHKOISLHYAFQ 50
DB 76 TGLPYGPGSAANFGNSNIGGEPPLNSVSPSLMLLHPPOSLPFLQPHQGVVYVINE 135
QY 51 KSPWC--EARSLEHTI PVNPEETLKPKVSNIPASPVTPGQ-----SKPFAHCAM:SOYA 103
DB 136 PSQTYVEAPAPPAVPP---NSINPRQDGERI ASTINDGSMAMEAKELRCVACVNOYA 192
QY 104 SGHYVWVSCFQKAFKPSLQGHNYTPATNCTLLNNPKNSQATLKVAYGVGV 162
DB 193 SGHYVWVSCFQKAFKPSLQGHNYTPATNCTLLNNPKNSQATLKVAYGVGV 162
QY 164 GQSPRPQCYRLVRPQSADEGHFQAGKAPRSZGHAPRV-----ELT 207
DB 253 GQIPKRPQPGPMKHKRQPRD-----GPGAGFVSNQGMVANI WSPPLMTPSKNSIA 307
QY 208 DALSPEDLVITLFAFPPHVISR--PSAPFTASMMMSITRIASKEIVHMSWAKETG 265
DB 308 LSLIADQVSAALIAAEP--ILYSEYDPTKPSVAMMILINADQETVHMINMAKRVG 366
QY 266 FVPLSLFDQVRLFSCMENVIMKIMKRSIDHPCKLIFADQVLDDBKCVGILTFD 425
DB 367 FVPLSLFDQVRLFSCMENVIMKIMKRSIDHPCKLIFADQVLDDBKCVGILTFD 425
QY 426 MLATTSRPPEIKQHEVYGVKAMILLNSMTYVAT QVANDSEKILANINVTAT 484
DB 427 MLATTSRPPEIKQHEVYGVKAMILLNSMTYVAT QVANDSEKILANINVTAT 484
QY 385 VVVIKAKSGISSQVSMKLANILMLSHVHASKKQEHILNMKKNVAVYELLEMLNA 444
DB 487 IHMAKAGLILQVCHQALADULLSHIHMSNPTMHYHSMQVAVVIVLEMLIA 546
QY 445 HVL 447
DB 547 HVL 549
DB 547 HVL 549

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RESULT 35
AAC84506
ID AAC84506 standard; Protein: 595 AA.

AAC84506:
10-SEP-2001 (first entry)

Human oestrogen receptor alpha protein mutant K103P

Ligand dependent transcriptional factor; oestrogen receptor; PR; glucocorticoid receptor protein; GR; mineralocorticoid receptor protein; MR; peroxisome proliferator-activated receptor protein; PPAR; progesterone receptor protein; PR; progesterone X receptor protein; RXR; thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR; transactivation; Eralpha; breast cancer; mutant; mutant.

Homo sapiens.

MO200142307-A1.

14-JUN-2001.

01-DEC-2000; 2000MO-IP0853.

07-DEC-1999; 99JP-048022.

27-DEC-1999; 99JP-037067.

07-JUL-2000; 2000JP-020701.

21-JUL-2000; 2000JP-023058.

02-AUG-2000; 2000JP-0234053.

03-AUG-2000; 2000JP-0234560.

03-AUG-2000; 2000JP-0234561.

03-AUG-2000; 2000JP-0234563.

(SUMO) SUMITOMO CHEM CO LTD.

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PI Saito K, Ohe N, Satoh H;
XX WPL: 2001-36/86/38.
PI Ligand dependent transcriptional factors, nucleic acids encoding them
PI and cells comprising them and a specified reporter gene, useful for
PI screening agents for the treatment of breast cancer
XX Claim 15; Page 170-174; 276pp; English.
XX The present invention relates to ligand dependent transcriptional factors
XX including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
XX receptor protein (GR), mineralocorticoid receptor protein (MR),
XX peroxisome proliferator-activated receptor protein (PPAR), progesterone
XX receptor protein (PR), progesterone X receptor protein (RXR), thyroid hormone
XX acids encoding them and cells comprising them and a specified reporter
XX gene for the ligand dependent transcriptional factor. These proteins are
XX useful in the modulation of ligand dependent transcriptional factor
XX activity. The cells, mutant Eralpha and the polynucleotide encoding it
XX may be used in assays for facilitating analysing an activity for
XX transactivation of a reporter gene by a test Eralpha, for screening
XX mutant ligand dependent transcriptional factors for evaluating an
XX activity for transactivation of a reporter gene by a test Eralpha and/or
XX for screening a compound useful for treating a disorder of a mutant
XX Eralpha, especially breast cancer.
XX Sequence 595 AA:
SO

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Query Match 47.7%; Score 1204; DB 22; Length 595;
Best Local Similarity 59.9%; Pred. No. 120-105;
Matches 246; Conservative 91; Mismatches 162; Indels 54; Gaps 10;

```

QY 10 INLEGGPGRO-----ITSPVIMPTGHSPLIVVHKOISLHYAFQ 50
DB 76 TGLPYGPGSAANFGNSNIGGEPPLNSVSPSLMLLHPPOSLPFLQPHQGVVYVINE 135
QY 51 KSPWC--EARSLEHTI PVNPEETLKPKVSNIPASPVTPGQ-----SKPFAHCAM:SOYA 103
DB 136 PSQTYVEAPAPPAVPP---NSINPRQDGERI ASTINDGSMAMEAKELRCVACVNOYA 192
QY 104 SGHYVWVSCFQKAFKPSLQGHNYTPATNCTLLNNPKNSQATLKVAYGVGV 162
DB 193 SGHYVWVSCFQKAFKPSLQGHNYTPATNCTLLNNPKNSQATLKVAYGVGV 162
QY 164 GQSPRPQCYRLVRPQSADEGHFQAGKAPRSZGHAPRV-----ELT 207
DB 253 GQIPKRPQPGPMKHKRQPRD-----GPGAGFVSNQGMVANI WSPPLMTPSKNSIA 307
QY 208 DALSPEDLVITLFAFPPHVISR--PSAPFTASMMMSITRIASKEIVHMSWAKETG 265
DB 308 LSLIADQVSAALIAAEP--ILYSEYDPTKPSVAMMILINADQETVHMINMAKRVG 366
QY 266 FVPLSLFDQVRLFSCMENVIMKIMKRSIDHPCKLIFADQVLDDBKCVGILTFD 425
DB 367 FVPLSLFDQVRLFSCMENVIMKIMKRSIDHPCKLIFADQVLDDBKCVGILTFD 425
QY 426 MLATTSRPPEIKQHEVYGVKAMILLNSMTYVAT QVANDSEKILANINVTAT 484
DB 427 MLATTSRPPEIKQHEVYGVKAMILLNSMTYVAT QVANDSEKILANINVTAT 484
QY 385 VVVIKAKSGISSQVSMKLANILMLSHVHASKKQEHILNMKKNVAVYELLEMLNA 444
DB 487 IHMAKAGLILQVCHQALADULLSHIHMSNPTMHYHSMQVAVVIVLEMLIA 546
QY 445 HVL 447
DB 547 HVL 549

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RESULT 36
AAC84513
ID AAC84513 standard; Protein: 595 AA.

XX Claim 6: Page 131-132; 149pp; English.

XX The present sequence is the protein sequence of the human nuclear
XX oestrogen receptor alpha (1). The invention relates to a non-human
XX mammalian organism, especially a transgenic mouse, characterized in
XX that at least one cell comprises: (i) a fusion protein formed from
XX a recombinase (Cre), a hinge region (preferably human (1) D hinge),
XX and a modified ligand binding domain (LBD) of a nuclear oestrogen
XX receptor, especially human (1), its fragment or variant, and (ii)
XX one or more genes or DNA sequences of interest belonging to the
XX genome of the organism, into which one or more recombination sites
XX of the recombinase protein are inserted. The (2) :Rb domain is
XX preferably modified by a G521R, G400V, or M53A/L544A mutation.
XX The fusion protein has no inhibitory, or even zero, recombinase
XX activity in the presence of a natural ligand such as oestradiol,
XX but recombinase activity is induced by a small quantity of a
XX synthetic ligand that has antiestrogenic activity, e.g. tamoxifen
XX or 4-hydroxytamoxifen. The mammalian organism or its cells, such
XX as epidermal cells, hepatocytes or adipocytes, are useful in
XX carrying out a spatiotemporally controlled site-specific
XX recombination of a DNA sequence of interest in its natural
XX chromatin environment. It is also used in screening of medicaments
XX for pathological conditions associated with an alteration of the
XX expression and/or function of the DNA sequence of interest, such as
XX skin cancer, inflammation, diabetes, alopecia, obesity, or in
XX promoting hepatic regeneration.

XX Sequence: 595 AA.

Query Match: 47.7%; Score 1204; DB 23; Length 595;
Best Local Similarity: 50.7%; Pred. No. 1,2e-105;
Matches: 245; Conservative: 81; Mismatches: 102; Indels: 54; Gaps: 10;

UY 10 TNRHGRGQ-----TTSPNVIWPRPSH SP-VVHPSH SHI YAPRQ 50
DB 76 TRLPYGPGSEAAFGNSMGLGPPPLNSVSRPMLIHPPQLSPFLGQGVPPYLLNE 135
UY 51 KSPWC--EARSLEHTLVNPFILKRVSNRCASPTGCG--SKRAHRCAGVSIVA 103
DB 136 PSYTVTFPAPPPAPYRP--NSQNPQGGSPPLASTNRKSGMAESAKETPPGAGVSNYA 192
UY 104 SCVHYVWSPCTCAFFRSTCTHNVTCTPATWCTTCCNPPSCVAPLPPYEVZWY 163
DB 193 SCVHYVWSPCTCAFFRSTCTHNVTCTPATWCTTCCNPPSCVAPLPPYEVZWY 252
UY 164 CTSRPPGCVPIVPPGPSARFQIHCACAKRSCGQANVPYR...P11L 207
DB 253 CGLPKRPPGCVPIVPPGPSARFQIHCACAKRSCGQANVPYR...P11L 207
UY 208 DALSPEQVLTLLAEPPHVLISR--PSAPFTASMMSTLTKLAEKELVHMSMKKRIHG 265
DB 308 LSLCAGQVMSALLDAEPP-ILYSEYDPTRFSSANSMMGLTINADDELVHMINNAKRVIG 366
UY 266 FVEISLFDQVPLPSWMEVLMKMLMPPSTIDHPGKILFAPDVLDDERKCEVEGILEPFD 325
DB 367 FVDITLHGVNHTFCAMFTILMIGVWPSMFHPCKILFADNILLTENCCKCEWCEWTEPFD 424
UY 325 MLATTSRRELKIQKRFYGVKAMILNSMYPVTAL--GQADSAPKLAHLINVTAL 384
DB 427 MLATTSRREPMNIQCFEYVGLKSTILENSGYTFTSTLKSLEKEKIHIVVGLTDL 486
UY 385 VWVIAKSGTSSQSSMFIANTIMLSHVPRASNKSEHILNNKCAWVVDVLLLEMA 444
DB 487 ILMIAKRGITLQDQHPALADLIITISHIRMSNKRMPHIYSMKCKVAVLETLLEMLIA 544
UY 445 HVL 447
DB 547 HRL 549

RESULT 38
AAG84512

11) AAG84512 standard; Protein: 595 AA.

XX AAG84512;

DT 10-SEP-2001 (1st entry)

DE Human oestrogen receptor alpha protein mutant K53H.

XX Ligand dependent transcriptional factor, oestrogen receptor; ER;
XX glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
XX MR; peroxisome proliferator-activated receptor protein; PPAR;
XX progesterone receptor protein; PR; pregnane X receptor protein; PXR;
XX thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
XX transactivation; Eralpha; breast cancer; mutant; metelin.

XX Homo sapiens.

XX W0200142407-A1.

XX 14-JUN-2001.

XX 01-DEC-2000; 2000W0-JP08553.

XX 07-DEC-1999; 99JP-0348022.

XX 27-DEC-1999; 99JP-0370667.

XX 07-JUL-2000; 2000JP-0307011.

XX 21-JUL-2000; 2000JP-020508.

XX 02-APR-2000; 2000JP-0234053.

XX 03-APR-2000; 2000JP-0234460.

XX 03-APR-2000; 2000JP-0235461.

XX 03-APR-2000; 2000JP-0235463.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX Saito K, Ohe N, Satoh H;

XX WPI: 2001-367866/38.

XX Ligand dependent transcriptional factors, nucleic acids encoding them
XX and cells comprising them and a specified reporter gene, useful for
XX screening agents for the treatment of breast cancer.

XX Disclosure: Page 191-194; 276pp; English.

XX The present invention relates to ligand dependent transcriptional factors
XX including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
XX receptor protein (GR), mineralocorticoid receptor protein (MR),
XX peroxisome proliferator-activated receptor protein (PPAR), progesterone
XX receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
XX receptor protein (TR) and vitamin D receptor protein (VDR). The nucleic
XX acids encoding them and cells comprising them and a specified reporter
XX gene for the ligand dependent transcriptional factor. These proteins are
XX useful in the modulation of ligand dependent transcriptional factor
XX activity. The cells, mutant Eralpha and the polynucleotide encoding it
XX may be used in assays for qualitatively analysing an activity for
XX transactivation of a reporter gene by a test Eralpha, for screening
XX mutant ligand dependent transcriptional factors, for evaluating an
XX activity for transactivation of a reporter gene by a test Eralpha and/or
XX for screening a compound useful for treating a disorder of a mutant
XX Eralpha, especially breast cancer.

XX Sequence: 595 AA;

XX Query Match: 47.7%; Score 1202; DB 22; Length 595;

XX Best Local Similarity: 50.7%; Pred. No. 1.4e-105;

XX Matches: 245; Conservative: 82; Mismatches: 102; Indels: 54; Gaps: 10;

UY 10 TNRHGRGQ-----TTSPNVIWPRPSH SP-VVHPSH SHI YAPRQ 50
DB 76 TRLPYGPGSEAAFGNSMGLGPPPLNSVSRPMLIHPPQLSPFLGQGVPPYLLNE 135
UY 51 KSPWC--EARSLEHTLVNPFILKRVSNRCASPTGCG--SKRAHRCAGVSIVA 103


```

DB 146 PSTYVWEAGNPVAYRP NSINRKGQBERLASTNKGSMAMESAKETRYAV-NYA 192
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DB 193 SGRHYGVWSEFGKAFKPKRSIGCHNDYICVAINMCTIDNKRKSSVACWLRGCVGVGMR 252
GY 164 GSRREKGVYVLYVHQSADQDHCACAKRSQSHAPVY-----EELL 207
DB 253 GGLRKRGRGRMLKHKHQDQD-----GEGRGVSGADHKAANIWSPIMKRKKNLSA 407
GY 208 DALSPEDVYLLEAEYVHLISK--PSAFTFASMMKSLTKAKELVHMLSMKRTG 265
DB 408 LSLADQVSNLLDAEPP--LLYSYEDPTREPSASMGILTNLADEIVHMINAKRVG 466
GY 266 FVELSLDGVYLLPESWMPVIMMGTMMPSLIGHKELFAPDVLIDDEKCVGCLLEFP 425
DB 467 FVDTLIDGVHLLPCLAMLETLMLGIVWRSVEHNGKLLFAPNILLDNQOKVGVGVELFD 426
GY 426 MLATTSRPRELKQHKRYLAVKAMILLNSMPTLVAT--QVADSSKRLAHLINAVTAL 484
DB 427 MLATSSRFPMNNLQGEFEVTKSLILNSVYTPSLTKSLERKQTHVLDKLTDTL 486
GY 485 VWVIAKSGTSSQGSMLANIMLSHVRASRCKMEHLINMKRVNVVYDILLPMLNA 444
DB 487 IHLMAKAGLTLQDQHRLAQLLLLSHDKMSKRMDEHLYSMKCNVNVLYDILLPMLNA 546
GY 445 HVL 447
DB 547 HRL 549

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RESULT 49

AA084507
ID AA084507 standard: protein: 595 AA.

AC AA084507:

DT 10 SEP 2001 (first entry)

XX Human oestrogen receptor alpha protein mutant S409F.

XX Ligand dependent transcriptional factor: oestrogen receptor; ER;
XX glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
XX MR; peroxisome proliferator-activated receptor protein; PPAR;
XX progesterone receptor protein; PR; vitamin X receptor protein; RX;
XX thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
XX Transactivation; Eralpha; breast cancer; mutant; meta.

XX Homo sapiens

UN W0200142407 AL.

XX 14-JUN 2001.

XX 01 DEC 2000; 2000WO-DE08553.

XX 07 DEC 1999; 99JP 0448022.

XX 27 DEC 1999; 99JP 0970667.

XX 07-JUN 2000; 2000JP-0207011.

XX 21 JUN 2000; 2000JP-0220598.

XX 02 AUG 2000; 2000JP-0244053.

XX 03 AUG 2000; 2000JP-0245460.

XX 03 AUG 2000; 2000JP-0245461.

XX 03 AUG 2000; 2000JP 0245464.

XX (SOMO) SUMITOMO CHEM CO LTD.

XX Saito K, Ghe N, Saitoh H.

XX WPI: 2001 467866/38.

XX Ligand dependent transcriptional factors, nucleic acids encoding them
XX and cells comprising them and a specified reporter gene, useful for
XX

PI screening agents for the treatment of breast cancer -
XX claim 16; page 174-177; 276pp; English.

XX The present invention relates to ligand dependent transcriptional factors
XX including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
XX receptor protein (GR), mineralocorticoid receptor protein (MR),
XX peroxisome proliferator-activated receptor protein (PPAR), progesterone
XX receptor protein (PR), progane X receptor protein (PRX), thyroid hormone
XX receptor protein (TR) and vitamin D receptor protein (VDR). The nucleic
XX acids encoding them and cells comprising them and a specified reporter
XX gene for the ligand dependent transcriptional factor. These proteins are
XX useful in the modulation of ligand dependent transcriptional factor
XX activity. The cells, mutant Eralpha and the polynucleotide encoding it
XX may be used in assays for qualitatively analysing an activity for
XX transactivation of a reporter gene by a test Eralpha, for screening an
XX mutant ligand dependent transcriptional factors, for evaluating an
XX activity for transactivation of a reporter gene by a test Eralpha and/or
XX for screening a compound useful for treating a disorder of a mutant
XX Eralpha, especially breast cancer.

XX Sequence 595 AA:

Query Match 47.6%; Score 1201; DB 22; Length 595;

Best Local Similarity 50.9%; Pred. No. 2; Ae 105;

Matches 246; Conservative 80; Mismatches 103; Indels 54; Gaps 10;

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GY 51 KSIWG--EASLEHLVLVNRRTKRVSNRCAVPTGQ--SKRIAHVAV-SOVA 103
DB 136 PSTYVWEAGNPVAYRP--NSINRKGQBERLASTNKGSMAMESAKETRYAV-NYA 192
GY 104 SGLHYGVWSEFGKAFKPKRSIGCHNDYICVAINMCTIDNKRKSSVACWLRGCVGVGMR 163
DB 193 SGRHYGVWSEFGKAFKPKRSIGCHNDYICVAINMCTIDNKRKSSVACWLRGCVGVGMR 252
GY 164 GSRREKGVYVLYVHQSADQDHCACAKRSQSHAPVY-----EELL 207
DB 253 GGLRKRGRGRMLKHKHQDQD-----GEGRGVSGADHKAANIWSPIMKRKKNLSA 407
GY 208 DALSPEDVYLLEAEYVHLISK--PSAFTFASMMKSLTKAKELVHMLSMKRTG 265
DB 408 LSLADQVSNLLDAEPP--LLYSYEDPTREPSASMGILTNLADEIVHMINAKRVG 466
GY 266 FVELSLDGVYLLPESWMPVIMMGTMMPSLIGHKELFAPDVLIDDEKCVGCLLEFP 425
DB 467 FVDTLIDGVHLLPCLAMLETLMLGIVWRSVEHNGKLLFAPNILLDNQOKVGVGVELFD 426
GY 426 MLATTSRPRELKQHKRYLAVKAMILLNSMPTLVAT--QVADSSKRLAHLINAVTAL 484
DB 427 MLATSSRFPMNNLQGEFEVTKSLILNSVYTPSLTKSLERKQTHVLDKLTDTL 486
GY 485 VWVIAKSGTSSQGSMLANIMLSHVRASRCKMEHLINMKRVNVVYDILLPMLNA 444
DB 487 IHLMAKAGLTLQDQHRLAQLLLLSHDKMSKRMDEHLYSMKCNVNVLYDILLPMLNA 546
GY 445 HVL 447
DB 547 HRL 549

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RESULT 40

AA084508
ID AA084508 standard: protein: 595 AA.

AC AA084508:

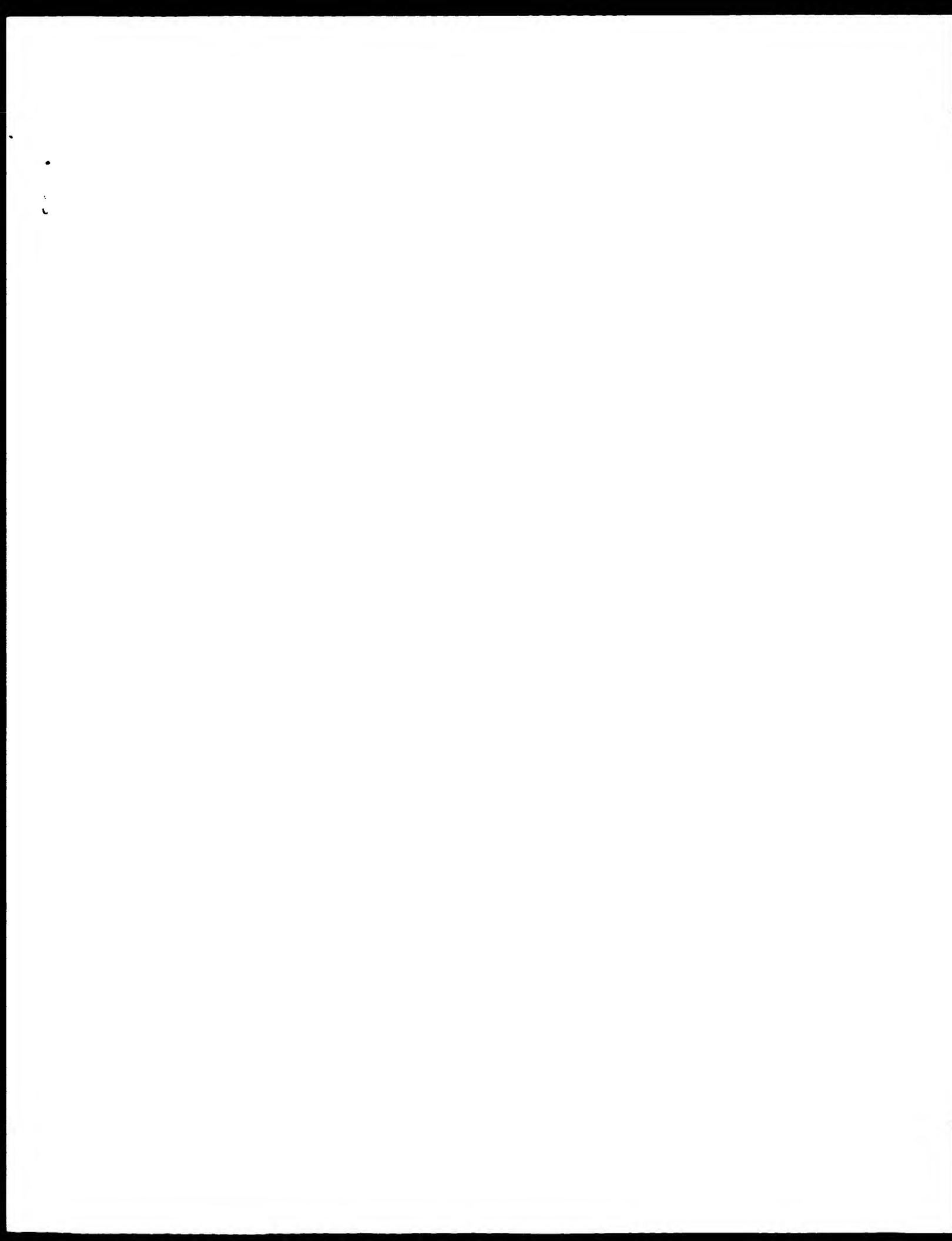
DT 10 SEP 2001 (first entry)

XX Human oestrogen receptor alpha protein mutant G590D.

XX Ligated dependent transcriptional factor: oestrogen receptor, PR
 XX glucocorticoid receptor protein, GR; mineralocorticoid receptor protein;
 KW MHC peroxisome proliferator-activated receptor protein, PPAR;
 KW Progesterone receptor protein, PR; progesterone X receptor protein, PRX;
 KW thyroid hormone receptor protein, TR; vitamin D receptor protein, VDR;
 KW transactivation; Eralpha; breast cancer; mutant; mutin.
 XX
 OS Homo sapiens.
 XX
 PN W0200142307-A1.
 PD 14-JUN-2001.
 XX
 PF 01-DEC-2000; 2000MC-IP08553
 XX
 PR 07-DEC-1999; 99JP-0348022.
 PR 27-DEC-1999; 99JP-0370667.
 PR 07-JUL-2000; 2000JP-0207011.
 PR 21-JUL-2000; 2000JP-0220508.
 PR 02-AUG-2000; 2000JP-0234053.
 PR 04-AUG-2000; 2000JP-0235460.
 PR 04-AUG-2000; 2000JP-0235461.
 PR 04-AUG-2000; 2000JP-0235463.
 XX
 PA (SUMO) SUMITOMO CHEM CO LTD.
 XX
 PI Saito K, Ohe N, Sato H;
 XX
 DR WPI: 2001-367866/38.
 XX
 PT Ligated dependent transcriptional factors, nucleic acids encoding them
 PT and cells comprising them and a specified reporter gene, useful for
 PI screening agents for the treatment of breast cancer -
 XX
 PS Claim 17; Page 177-180; 276pp; English.
 XX
 CC The present invention relates to ligand dependent transcriptional factors
 CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
 CC receptor protein (GR), mineralocorticoid receptor protein (MR),
 CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
 CC receptor protein (PR), progesterone X receptor protein (PRX), thyroid hormone
 CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
 CC acids encoding them and cells comprising them and a specified reporter
 CC gene for the ligand dependent transcriptional factor. These proteins are
 CC useful in the modulation of ligand dependent transcriptional factor
 CC activity. The cells, mutant Eralpha and the polynucleotide encoding it
 CC may be used in assays for qualitatively analysing an activity for
 CC transactivation of a reporter gene by a test Eralpha, for screening
 CC mutant ligand dependent transcriptional factors, for evaluating an
 CC activity for transactivation of a reporter gene by a test Eralpha and/or
 CC for screening a compound useful for treating a disorder of a mutant
 CC Eralpha, especially breast cancer.
 CC
 XX
 SQ Sequence 595 AA;
 Query Match 47.5%; Score 1197; DB 22; Length 595;
 Best Local Similarity 50.7%; Pred. No. 5,5e-105;
 Matches 245; Conservative 81; Mismatches 103; Indels 54; Gaps 10;
 QY 10 TLEGGDGRQ-----TSPNVLMPTPGHLSL-LVHRLSHLYARPD 50
 DB 76 TGLPYGPGSLAAAGSGNGLGFPPLNSVSPSLMLHPPLSLPJOHCOOVPEYLENE 135
 QY 51 KSPWC--EARSLEHTLIPVNPFTLKHKVSNPCASPYTSG-----SKRDHFCAVCSQYA 103
 DB 136 PSCTVTPPACPAVFP---NQNPPGCTPPPLASTNKGSMAMESAEETFCVCAVCSQYA 192
 QY 104 STYHYGVASCTFGCAKPKPSIQSHNDYTPPATNCTIDFNPKSCQACGLPRCYEV2MYK 163
 DB 193 STYHYGVASCTFGCAKPKPSIQSHNDYTPPATNCTIDFNPKPSQACGLPRCYEV2MYK 252
 QY 164 GTSPPPPGCTRIIVPPPSANPOLHCAKPKSG3HAPVP-----ELLT 207

Ph 253 GATFRGSGSPMLKRFSLHFD... GGGGGLVSGAGGMAANLMPSTLTKSKKNSIA 307
 QY 208 DATSPQELVTLLEAFPRVLSR--PSAPFEASMMMLTRLAPELVHMSAEPFPG 265
 Ph 308 LSTATGVMSALTFAPFP--TYSFTPTPPPSFASMMMLTNIADRIVHIMNAKVPV 366
 QY 266 FVFTSI FEGVPLESTWMEVLMMLIMWSHHPGKIIPAPDVLTLGPRKVPF11FFD 325
 DB 367 FVDFTI HQGVHILFVAMLETIMDIWPSMEHPGKIFAPN11DRWQKCVGMPVE1FFD 426
 QY 326 MLATTSRRELKLOHKEYLGVKAMILLNSVYPLVAT--ODADSRKLAHLAAV1DAL 384
 DB 427 MLATTSRFRMMNLGSEFVCLKSTILLNSGYTTLSTLKSLEKIH1HVLK1D1L 486
 QY 385 VWYIARSGTSSQGSVMRIANILLSHYHASNKGMPIIMKCKNNVAVYH1LEM1NA 444
 DB 487 IHMAKAGL1LQDQHGLAQLLLLSH1RHMSNKGMEHL1SMKCKNNVAVYD1LEM1DA 546
 QY 445 HVL 447
 DB 547 HRL 549

Search completed: June 16, 2003, 13:12:47
 Job time : 128.703 secs



GenBore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:13:43 : Search time 23.4645 seconds

(without alignments)
598.126 Million cell updates/sec

Title: US-08-826-361A-5

Perfect score: 25222

Sequence: 1 MNTSIPSNVTNI P3306PCT

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 26422922 residues

Total number of hits satisfying chosen parameters: 262774

Minimum hit seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 120 summaries

Database : Issued Patents_AA*

1: /patent/epubdata/1/144/5A/0266.pat *

2: /patent/epubdata/1/144/5A/0266.pat *

3: /patent/epubdata/1/144/5A/0266.pat *

4: /patent/epubdata/1/144/5A/0266.pat *

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6: /patent/epubdata/1/144/5A/0266.pat *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2522	100.0	548	4	US-09-119-617-1
2	2522	100.0	548	4	US-09-551-741A-1
3	2512	99.6	485	2	US-08-846-620A-3
4	2349	89.2	484	2	US-08-846-620A-2
5	2349	89.0	484	2	US-08-846-620A-13
6	2330	88.4	485	2	US-08-846-620A-5
7	2225	88.2	484	2	US-08-846-620A-14
8	2017	80.9	384	2	US-08-846-620A-15
9	1204	47.7	595	4	US-08-764-870-12
10	1204	47.7	595	4	US-08-764-870-12
11	1195	47.4	595	4	US-09-041-886-45
12	1195	47.4	595	4	US-09-041-886-45
13	1193	47.3	591	2	US-08-846-620A-17
14	1192.5	47.3	592	2	US-08-846-620A-16
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16	1126.5	44.7	229	4	US-09-249-645-1
17	1064	42.2	228	4	US-09-249-645-2
18	1055	41.8	226	2	US-08-836-620A-7
19	796	31.6	773	3	US-08-564-264-1
20	762	30.2	651	4	US-08-694-940-1
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22	668.5	26.5	243	2	US-08-846-620A-9
23	660.5	26.4	243	2	US-08-846-620A-8
24	660.5	26.4	243	2	US-08-846-620A-10
25	644.5	26.6	435	3	US-09-041-886-45
26	644.5	26.6	435	3	US-09-041-886-45
27	644.5	26.6	435	3	US-09-041-886-45
28	630	25.0	500	3	US-09-141-000-2
29	626	24.8	441	2	US-08-846-620A-19
30	595.5	23.2	518	2	US-08-846-620A-18
31	572.5	22.7	418	3	US-09-141-000-6
32	460.5	18.3	525	4	US-08-764-870-7
33	460.5	18.3	525	4	US-08-764-870-7
34	458.5	18.2	534	1	US-07-952-800-2
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67	383	15.2	495	3	US-09-282-803B-2
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US-08-836-620A-3
Sequence 3, Application US/08846620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08-836-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/09949
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607542.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-836-620A-3

Query Match 99.6% Score 2512; DB 2; Length 485;
Best Local Similarity 99.8%; Pctid No 1 99-264;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 9 MNYSIPSNVTNLBGGPGRQTTSPNVLMPTFGHLSPIVHROUSHLAEPQKSWCFARSL 68
QY 61 EHTLPVNRFTLKRKVSNGRCASPVTPGSKRDAHFVAVSDVASYHYGVMSCEGKAEF 120
DB 69 EHTLPVNRFTLKRKVSNGRCASPVTPGSKRDAHFVAVSDVASYHYGVMSCEGKAEF 128
QY 121 KRSTGGNDVYCPATNCTTIDKRPKSGVACPIKCYEVGVAVGCSPPRECVPIVPPGR 180
DB 129 KRSTGGNDVYCPATNCTTIDKRPKSGVACPIKCYEVGVAVGCSPPRECVPIVPPGR 188
QY 181 SADBQJHCAKAKSASHAPVPELLDALSPQLVLTLEAPPHVLSRSPAPTEAS 240
DB 189 SADBQJHCAKAKSASHAPVPELLDALSPQLVLTLEAPPHVLSRSPAPTEAS 248
QY 241 MMSSTIKAEKELVHMTSMARKIPGEVELSLFVQVRLTESQWMEVLMMSIHHPRK 300
DB 249 MMSSTIKAEKELVHMTSMARKIPGEVELSLFVQVRLTESQWMEVLMMSIHHPRK 308
QY 401 LIFAPADVLDPEPKCVPGILLFTDMLATTSPEPELKQHKRYLVKAMILLNSMYPL 460
DB 409 LIFAPADVLDPEPKCVPGILLFTDMLATTSPEPELKQHKRYLVKAMILLNSMYPL 468
QY 461 VTATGADSSKRLAHLNAVTDALVWYIAKSGISSQGSMBRLANLMLSHVHASNKM 420
DB 469 VTATGADSSKRLAHLNAVTDALVWYIAKSGISSQGSMBRLANLMLSHVHASNKM 428
QY 421 EHLNMMKGNVVEYDILLFELNNAVILJGCKSSITSGCSPADSKSKESQNSQSD 477
DB 429 EHLNMMKGNVVEYDILLFELNNAVILJGCKSSITSGCSPADSKSKESQNSQSD 485

RESULT 4
US-08-836-620A-2
Sequence 2, Application US/08846620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-836-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/09949
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607542.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-2

Query Match 89.2% Score 2249; DB 2; Length 485;
Best Local Similarity 88.5%; Pctid No 7 76-236;
Matches 422; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

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DB 9 MNYSIPSNVTNLBGGPGRQTTSPNVLMPTFGHLSPIVHROUSHLAEPQKSWCFARSL 68
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DB 69 EHTLPVNRFTLKRKVSNGRCASPVTPGSKRDAHFVAVSDVASYHYGVMSCEGKAEF 128
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DB 409 LIFAPADVLDPEPKCVPGILLFTDMLATTSPEPELKQHKRYLVKAMILLNSMYPL 468
QY 461 VTATGADSSKRLAHLNAVTDALVWYIAKSGISSQGSMBRLANLMLSHVHASNKM 420
DB 469 VTATGADSSKRLAHLNAVTDALVWYIAKSGISSQGSMBRLANLMLSHVHASNKM 428

106 LIFAPDLVLRDEKCEVEEILETFIMLATAFPELKIQREKYLQKAMILLNSMYH 468
QY 461 VTATQADSSKRLAHILNATDIALVWIAKSGISSQOOSMRANILMLSHVHASNKM 420
106 469 ATASQAFSSKRLTHIINATDIALVWIAKSGISSQOOSMRANILMLSHVHASNKM 428
QY 421 FHILNMCKRVVYVYIILEMNAHIFQKRSSTGSGGCTEDSKSKSGSONLQSO 477
106 429 FHILSMCKRVVYVYIILEMNAHILKQKRSSTGSGGCTEDSKSKSGSONLQSO 485

RESULT 7
US-08-836-620A-14
Sequence 14, Application US/08846620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPI)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-836-620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03033
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607542.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-836-620A-14

Query Match: 88.2%; Score 2255; DB 2; Length 484,
Post local similarity 88.0%; Prod. No. 3.1e-213;
Matches 419; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

QY 1 MNTSPNSVNTNPGSPGPTTSPNVLMPTPHLSPLVHROLSHLAEPQKSIWPAEEL 60
106 9 MNTSPNSVNTNPGSPGPTTSPNVLMPTPHLSPLVHROLSHLAEPQKSIWPAEEL 68
QY 61 FHITPVNPEHKKPVKSPASPVYTGSGPRDHPFCAVSDVAGSHYGVWVSGEYKAF 120
106 69 FHITPVNPEHKKPVKSPASPVYTGSGPRDHPFCAVSDVAGSHYGVWVSGEYKAF 128
QY 121 KASTGHNQYTPATNCTTGNPPSPVATFAPVYVWVWVWVWVWVWVWVWVWVWVWV 180
106 129 KSTGHNQYTPATNCTTGNPPSPVATFAPVYVWVWVWVWVWVWVWVWVWVWVWV 188
QY 181 SADIOLGACAKKSGSHARVRELLDALSPQLVITLHAPPPVILSRSPAPTEAS 240
106 189 SASDVOLGAKKSGSHARVRELLDALSPQLVITLHAPPPVILSRSPAPTEAS 248
QY 241 MMSLTKLAKREIVHIMISWAKKIPGVETSLFQVRLLESCWMEVIMMGIWMSIHNGK 400
106 249 MMSLTKLAKREIVHIMISWAKKIPGVETSLFQVRLLESCWMEVIMMGIWMSIHNGK 408

QY 301 LIFAPDLVLRDEKCEVEEILETFIMLATAFPELKIQREKYLQKAMILLNSMYH 460
106 469 LIFAPDLVLRDEKCEVEEILETFIMLATAFPELKIQREKYLQKAMILLNSMYH 468
QY 361 VTATQADSSKRLAHILNATDIALVWIAKSGISSQOOSMRANILMLSHVHASNKM 420
106 369 ATASQAFSSKRLTHIINATDIALVWIAKSGISSQOOSMRANILMLSHVHASNKM 428
QY 421 FHILNMCKRVVYVYIILEMNAHIFQKRSSTGSGGCTEDSKSKSGSONLQSO 476
106 429 FHILSMCKRVVYVYIILEMNAHILKQKRSSTGSGGCTEDSKSKSGSONLQSO 484

RESULT 8
US-08-836-620A-15
Sequence 15, Application US/08846620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPI)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03033
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607542.0
FILING DATE: 11-APR-1996
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-836-620A-15

Query Match: 80.0%; Score 2017; DB 2; Length 484,
Post local similarity 100.0%; Prod. No. 9.2e-211;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LSPVHROLSHLAEPQKSIWPAEELTHLVNPEHKKPVKSPASPVYTGSGPRD 92
106 2 LSPVHROLSHLAEPQKSIWPAEELTHLVNPEHKKPVKSPASPVYTGSGPRD 61
QY 93 AHFCAVSDVAGSHYGVWV 152
106 62 AHFCAVSDVAGSHYGVWV 121
QY 153 LKRYEYVWV 212
106 122 LKRYEYVWV 181
QY 213 EQLVILHAPPPVILSRSPAPTEASMMMSILKADPEVHIMISWAKKIPGVETSLF 272
106 182 EQLVILHAPPPVILSRSPAPTEASMMMSILKADPEVHIMISWAKKIPGVETSLF 241

Query Match	47.7%	Score	1204	184	Length	595	
Best Local Similarity	50.9%	Pred. No.	5	40	122		
Matches	246	Conservative	81	Mismatches	102		
				Indels	54	Gaps	19

10 INLENGPFO-----TTSNVLWPTGHLSTLWVHQLSHLYAHQ 50
 | | | | | | | | | | |
76 TELLYGDSFMAAHSNMLHPPELVSVNSLTMLHPPLSPFLPHCGVVYTLNH 145
 | | | | | | | | | | | |
51 KSDWV--EAPSLPIITDVNLFTIKKVSINCPASGVDTQ---SPDQAHCNVAGVA 103

104	SYBERGWSTGCKKAPFKRSTQGHNOYTOPA.NUUTIKRNPKNVACNPJPKVEVZYWK	16.3
146	PSYTYVPPAPAPAPYp- - - NSNINPpLpLpPLASTINPKRQMAHSAKRYBYVAVNYVA	19.2
150	-----	19.5
151	-----	19.5
152	-----	19.5
153	-----	19.5
154	-----	19.5
155	-----	19.5
156	-----	19.5
157	-----	19.5
158	-----	19.5
159	-----	19.5
160	-----	19.5
161	-----	19.5
162	-----	19.5
163	-----	19.5
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167	-----	19.5
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171	-----	19.5
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173	-----	19.5
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198	-----	19.5
199	-----	19.5
200	-----	19.5

[illegible]

208 DALSDEQVITILFAHPHVLISR - PSAPTEASMMSLIKLNLNVIIMSWAK IIIG 265
:: ::
308 ESTADGVNSALLAEPY- ILYSEYPDIFKEEASMGLTINLAIREI VIMI IWARKVE? 346

[illegible]

427 MLATSSFFRRMNIQCHPEVOTFSTIIILNSNYTHLSSTKLEPPQHPHFVLEKLTDDI 486
385 VVVFARSTSSQLQSMETANIMLSHVHASNKMEDLLMKSKKNVAVPYLLLEELNNA 444

487. IHLMAKATITITQ22H0R1A01L1LSH1PHMSNKK2MEHLYSMKKKNVPP1YDLLEENJA 546
y 445 HVL 447
1 1
547 HRL 549

ESTT 11
S-09-041-886-45
Sequencer 45, Application US75941886

Patent No. 6,258,72

GENERAL INFORMATION:

APPLICANT: Bredesen, Dale E.

INVENTOR: Rabinzadeh, Sharron

TITLE OF INVENTION: proapoptotic peptides, dependence

TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Fioresi LLP
STREET: 4170 La Jolla Village Drive, Suite 700

CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compat file
OPERATING SYSTEM: PC/IOS/MS-DOS
SOFTWARE: Patent in Release #1 0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09/041,880
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 41,815
REFERENCE/ORDER NUMBER: P-41 27-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ. NO.: 45;
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids

: **FUNCTION:** amino acid
 : **TYPE:** amino acid
 : **TOPOLOGY:** linear
 : **MOLECULE TYPE:** protein
 US-09-041-886 35

Query Match	47.48	Score 1195	DB 4	Length 595
Best Local Similarity	50.7%	Prod. No. 5.2e11		
Matches 245	Conservative 81	Mismatches 133	Indels 54	Gaps 10

51 KSDW--EAPSLFHITPVNPFLLKKVKSINQASVTPGPT-----SKIDHHPAAGVSQYA 103

130 PSQVYVPEKAPAPAPPP--NSQNPQGGPPIASTNPKSSMMHSEKREYAVVNDYA 192

[illegible]

07	200	HALSPOLVITLHAPHVLS--PSAFTESMSSTKADPELVMSMAKING	265
08	408	1STFAOMSAIDAPD--1LYSEYDIPRPSMSMGLINADRELVIMINWARVC	466
09	266	1VELSTEDVECTSTWELVEMOLMWSCTHPSKLEFAPVIMDEPZVAGVLEHTH	625

367 FVDTLTHDVHLLCEMALEITLMTGLVHPSMHPKLLFARNLLPDRNGKCYVSGMPFED 426
DY MLATTSRFRPKIQHREYCYVKAMLLNSSMPYLVATQDAUSRKLAKLLNAVTDAL 384

```

100 4 2 2 M L A T S R F R P M N M L J C H E E V C K S T I L D N S V Y F L E S T K S L E E K H I H V A T K I T D I L 486
097 185 V W V I A N S G I S Y G G S R H A N L M L S H V H A S N K M E H L I N M K K N V V Y D I L L E M I N A 444
096 I H M A A M L I L L C C H I R A L A L L I L S H I K P M S N M E H L S M K S N V A V Y D I L L E M I A 546

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QY	44.5	HVL	4.47
		—	—
RD	5.47	HVL	5.49

RESULT 12
US-08-453-998-2
Sequence 2, Application US/08453998
Patent No. 644438

GENERAL INFORMATION:
APPLICANT: CHAMHON, PIERRE
APPLICANT: METZGER, DANIEL
APPLICANT: WHITE, JOHN
TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROTEIN

1 TITLE OF INVENTION: HY YEASTS USING AN INHIBITILE SYSTEM, VECTORS AND
2 TITLE OF INVENTION: (CORRESPONDING TRANSFORMED STRAINS
3 NUMBER OF SEQUENCES: 15
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: CUSHMAN, BARRY & CUSHMAN

STREET: 1100 NEW YORK AVE., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: FLOPPY DISK
3  COMPUTER: IBM PC COMPATIBLE
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5

```


1 PRIOR APPLICATION NUMBER: GB 980 4062.0
 2 PRIOR FILING DATE: 1998-02-13
 3 NUMBER OF SEQ ID NOS: 2
 4 SEQUENCE: Post seq for Windows Version 4.0
 5 SEQ ID NO 1
 6 LENGTH: 229
 7 TYPE: PRT
 8 ORGANISM: Human
 9 US 09 249 645 1

Query Match 44.7% Score 1126.57 DB 4: Length 229;
 Best Local Similarity 96.0% Pctid No. 41 to 114;
 Matches 228; Conservative 0; Mismatches 1; Indels 11; Gaps 2;

0Y 408 DALSPGQVITTEAPPPVIVISPPSAPETASMMSTIKLAKKELVIMISMAKKEGV 267
 1 DALSPGQVITTEAPPPVIVISPPSAPETASMMSTIKLAKKELVIMISMAKKEGV 55
 0Y 268 PPSPPVPLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 427
 0Y 56 PPSPPVPLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 115
 0Y 428 LATSPPPEIKLQKREKIVKAMILNNSMYPIVTVGUDSSKELAHINVTDAVWV 487
 116 LATSPPPEIKLQKREKIVKAMILNNSMYPIVTVGUDSSKELAHINVTDAVWV 169
 0Y 408 LAKSSTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVVYVILLKEMNAVIL 447
 170 LAKSSTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVVYVILLKEMNAVIL 259

RESULT 17
 US 09 249 645 2
 1 Sequence 2: Application US/09249645
 2 Patent No. 6,230,990
 3 GENERAL INFORMATION:
 4 APPLICANT: Immunogen, Inc.
 5 APPLICANT: Boston, MA
 6 APPLICANT: Boston, MA
 7 APPLICANT: Boston, MA
 8 APPLICANT: Boston, MA
 9 APPLICANT: Boston, MA
 10 APPLICANT: Boston, MA
 11 APPLICANT: Boston, MA
 12 APPLICANT: Boston, MA
 13 APPLICANT: Boston, MA
 14 APPLICANT: Boston, MA
 15 APPLICANT: Boston, MA
 16 APPLICANT: Boston, MA
 17 APPLICANT: Boston, MA
 18 APPLICANT: Boston, MA
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 96 APPLICANT: Boston, MA
 97 APPLICANT: Boston, MA
 98 APPLICANT: Boston, MA
 99 APPLICANT: Boston, MA
 100 APPLICANT: Boston, MA

1 FILE REFERENCE: 101967 100
 2 CURRENT APPLICATION NUMBER: US/09/249, 645
 3 CURRENT FILING DATE: 1999-02-12
 4 PRIOR APPLICATION NUMBER: GB 980 4062.0
 5 PRIOR FILING DATE: 1998-02-13
 6 NUMBER OF SEQ ID NOS: 2
 7 SEQUENCE: Post seq for Windows Version 4.0
 8 SEQ ID NO 2
 9 LENGTH: 228
 10 TYPE: PRT
 11 ORGANISM: Rat
 12 US 09 249 645 2

Query Match 42.2% Score 1064; DB 4: Length 228;
 Best Local Similarity 96.2% Pctid No. 26 to 107;
 Matches 212; Conservative 8; Mismatches 7; Indels 8; Gaps 1;

0Y 216 LSPGQVITTEAPPPVIVISPPSAPETASMMSTIKLAKKELVIMISMAKKEGV 269
 1 LSPGQVITTEAPPPVIVISPPSAPETASMMSTIKLAKKELVIMISMAKKEGV 61
 0Y 270 SLFQVQLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 429
 1 SLFQVQLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 121
 0Y 62 SLFQVQLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 429
 1 SLFQVQLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 489
 0Y 122 PPSPPVPLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDKCVVPSLLEPDK 181

0Y 490 KSGTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVVYVILLKEMNAVIL 444
 1 KSGTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVVYVILLKEMNAVIL 228

RESULT 18
 US 08-826-620A 7
 1 Sequence 7: Application US/08826620A
 2 Patent No. 6,958,710
 3 GENERAL INFORMATION:
 4 APPLICANT:
 5 TITLE OF INVENTION: orphan receptor
 6 NUMBER OF SEQUENCES: 19
 7 COMPUTER READABLE FORM:
 8 MEDIUM TYPE: floppy disk
 9 OPERATING SYSTEM: PC-DOS/MS-DOS
 10 SOFTWARE: Patent In Rights #1.0, Version #1.25 (PRT)
 11 CURRENT APPLICATION DATA:
 12 APPLICATION NUMBER: US/08/826, 620A
 13 FILING DATE:
 14 PRIOR APPLICATION DATA:
 15 APPLICATION NUMBER: PCT/EP96/03933
 16 FILING DATE:
 17 APPLICATION NUMBER: GB 9518272.1
 18 FILING DATE: 08 SEP-1995
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER: GB 9605550.4
 21 FILING DATE: 15 MAR-1996
 22 PRIOR APPLICATION DATA:
 23 APPLICATION NUMBER: GB 9607542.0
 24 FILING DATE: 11 APR-1996
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: GB 9605576.5
 27 FILING DATE: 08 MAY-1996
 28 INFORMATION FOR SEQ ID NO: 7:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 226 amino acids
 31 TYPE: amino acid
 32 TOPOLOGY: linear
 33 ORIGINAL SOURCE:
 34 ORGANISM: Rattus rattus
 35 US 08-826-620A 7

Query Match 41.8% Score 1055; DB 2: Length 226;
 Best Local Similarity 91.2% Pctid No. 186-106;
 Matches 206; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

0Y 252 LLYVMSMAKKEGVVPEVLESLIDVQKLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDK 411
 1 LLYVMSMAKKEGVVPEVLESLIDVQKLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDK 60
 0Y 412 DEGRVQLESLIDVQKLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDK 471
 1 DEGRVQLESLIDVQKLESSWPEVLMKLMWSTIDPKELVAPPEVLEPDK 120
 0Y 472 KLAHILNAVITDAVWVIAKSTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVV 441
 1 KLAHILNAVITDAVWVIAKSTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVV 180
 0Y 121 KLAHILNAVITDAVWVIAKSTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVV 477
 1 KLAHILNAVITDAVWVIAKSTSSGQSMPLANIMLSHVPASNKIMHILNMGKGVAVV 226

RESULT 19
 US 08-564-264 1
 1 Sequence 1: Application US/08564264
 2 Patent No. 6,044,600
 3 GENERAL INFORMATION:
 4 APPLICANT: STEWART, FRANKS
 5 TITLE OF INVENTION: REGULATION OF SITE SPECIFIC

126 GINNYTADANOTITLIPNPKRSVACRPEVLSLPGVVLSP-PLPQAPVPSAN- 407
 135 GNTFYSPTATNECTTKRRKRSVACRPEKTKRVMKRGVLEKQVGRGGRGKRR- 194
 184 EOLARACKARSGSHARVR-ELLALASP-POLVLTLELAEPPV-LISRAAPTEAS 240
 195 -----NSPYLNPOLVQAPKRYNKTIVSHLLVADEPKIYAMPDPTVIDSDIK 243
 419 GMEHLNMRCKNVVYDILLEMNAHV 446
 408 AVQHPYMKLEKRVPMIRLLEMLAKV 435

RESULT 26
 US 09 500 654 2
 Sequence 2, Application US/09500654
 Patent No. 659116
 GENERAL INFORMATION:
 APPLICANT: Stephen L. Mathias
 TITLE OF INVENTION: No. 659116-1 Compounds
 FILE REFERENCE: GP 40008 D1
 CURRENT APPLICATION NUMBER: US/09/500,654
 CURRENT FILING DATE: 2000 02 09
 EARLIER APPLICATION NUMBER: 9/05451.4
 EARLIER FILING DATE: 1997 03 17
 EARLIER APPLICATION NUMBER: 9803289.9
 EARLIER FILING DATE: 1998-02-16
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 456
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US 09 500-654-2

Query Match 25.68: Score 644.5; ID 4; Length 456;
 Post Local Similarity 48.18; Pred. No. 2.5e-61;
 Matches 148; Conservative 82; Mismatches 117; Indels 41; Gaps 12;

135 GNTFYSPTATNECTTKRRKRSVACRPEKTKRVMKRGVLEKQVGRGGRGKRR- 194
 184 EOLARACKARSGSHARVR-ELLALASP-POLVLTLELAEPPV-LISRAAPTEAS 240
 195 -----NSPYLNPOLVQAPKRYNKTIVSHLLVADEPKIYAMPDPTVIDSDIK 243
 419 GMEHLNMRCKNVVYDILLEMNAHV 446
 408 AVQHPYMKLEKRVPMIRLLEMLAKV 435

RESULT 26
 US 09 500 654 2
 Sequence 2, Application US/09500654
 Patent No. 659116
 GENERAL INFORMATION:
 APPLICANT: Stephen L. Mathias
 TITLE OF INVENTION: No. 659116-1 Compounds
 FILE REFERENCE: GP 40008 D1
 CURRENT APPLICATION NUMBER: US/09/500,654
 CURRENT FILING DATE: 2000 02 09
 EARLIER APPLICATION NUMBER: 9/05451.4
 EARLIER FILING DATE: 1997 03 17
 EARLIER APPLICATION NUMBER: 9803289.9
 EARLIER FILING DATE: 1998-02-16
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 456
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US 09 500-654-2

Query Match 25.68: Score 644.5; ID 4; Length 456;
 Post Local Similarity 48.18; Pred. No. 2.5e-61;
 Matches 148; Conservative 82; Mismatches 117; Indels 41; Gaps 12;

419 GMEHLNMRCKNVVYDILLEMNAHV 446
 408 AVQHPYMKLEKRVPMIRLLEMLAKV 435

RESULT 27
 US 09 141 000-4
 Sequence 4, Application US/09141000
 Patent No. 6054295
 GENERAL INFORMATION:
 APPLICANT: Chou, Fung
 TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
 TITLE OF INVENTION: RECEPTOR PROTEINS
 FILE REFERENCE: 199999
 CURRENT APPLICATION NUMBER: US/09/141,000
 CURRENT FILING DATE: 1998-08-26
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 456
 TYPE: PRT
 ORGANISM: Human
 US 09 141-000-4

Query Match 25.68: Score 644.5; ID 4; Length 456;
 Post Local Similarity 48.18; Pred. No. 2.7e-61;
 Matches 148; Conservative 82; Mismatches 117; Indels 41; Gaps 12;

419 GMEHLNMRCKNVVYDILLEMNAHV 446
 408 AVQHPYMKLEKRVPMIRLLEMLAKV 435

RESULT 27
 US 09 141 000-4
 Sequence 4, Application US/09141000
 Patent No. 6054295
 GENERAL INFORMATION:
 APPLICANT: Chou, Fung
 TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
 TITLE OF INVENTION: RECEPTOR PROTEINS
 FILE REFERENCE: 199999
 CURRENT APPLICATION NUMBER: US/09/141,000
 CURRENT FILING DATE: 1998-08-26
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2

Query Match 25.68: Score 644.5; ID 4; Length 456;
 Post Local Similarity 48.18; Pred. No. 2.7e-61;
 Matches 148; Conservative 82; Mismatches 117; Indels 41; Gaps 12;

UY 182 ADEQLHACKAKRSQGHAVRVELLDALSPQOL-VITLLEAPPHVLI----- 229
DB 277 KIDGDCAGCA-----PREMPDRILLEAE---LAVGKSDGQVGGP 314
UY 230 -----SPSAPPTASMMMSLTKLAWEFTVWMLSWAKIPGVEHSLFDVRLLESQW 282
DB 415 GGTGGSSSPNDPVT-----NIGQAARKQFTVWMAKIPHESSSLFDVRLLESQW 368
UY 283 MEVIMMOLMRSIDHCKIIFAPDVIIDPEKCVGHELEPDMILA-TTSPEPELKH 341
DB 369 NELLIASFSRSDIVPGCHILALGIVHNSASHA-GVGAIPDVI TELVSKMIPMBIK 427
UY 342 KEVLYKAMILLNSSMYPVTAIGVQALSSKRLAHINAVITAIWVIAVIAKSGISSQOSMR 401
DB 428 TELGCRALILFMDPAKGL-----SNPSEVEVLREKVASLETYCKOKYPPDOG--K 477
UY 402 LANIMLISHVRHASKRMCHILNMCKRVVVPYDILLEMNA 444
DB 478 FAKILLRLPALRSIGLKEHLPEFKLIGDTPIDITLMEMLFA 520

RESULT 34

US-08-980-115-7
Sequence 7, Application US/08980115
Patent No. 625622
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Flettyck, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Appleby, James W.
APPLICANT: West, Brian L.
APPLICANT: Shau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: OCAI: 246/0205
CURRENT APPLICATION NUMBER: US/08/980,115
EARLIER FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER FILING DATE: 1995-12-14
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,541
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (292)..(523)
OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-7

Query Match 18.3% Score 460.5; DB 4; Length 525;
Best Local Similarity 30.2%; Pred. No. 3,5e-41;
Matches 140; Conservative 51; Mismatches 165; Indels 97; Gaps 16.

UY 9 VTINLEGPBQHTSPNVIWPTPCHISPLVHPQLSHLVAPKSPWCEASLEHILPVN- 67
DB 128 ISSMSGSPGPPAP-----PG-----FSGVSSPDINSTV---SLPGG 164
UY 68 KEIKKRVSSNR CASPVIGSKRIAHAVAVSGVAGVYVWMSPPCKAFK 121
DB 165 SGPETVWKPPIVAVGRIHPPPPGACK--PI/CAICGIBSSGHEVYVSGEYCKGPK 222
UY 122 RSLGHNIVYCPATNPTTIKKKPKSGVAGPKPVAVWVQSPSPFPVGPVIVGK 161

DB 423 PIIPEHLLSSTPECHETVKEKPSHCHQVYVYEGCLALSPMPFVAPFPP- 276
UY 182 ADEQLHACKAKRSQGHAVRVELLDALSPQOL-VITLLEAPPHVLI----- 229
DB 277 KIDGDCAGCA-----PREMPDRILLEAE---LAVGKSDGQVGGP 314
UY 230 -----SPSAPPTASMMMSLTKLAWEFTVWMLSWAKIPGVEHSLFDVRLLESQW 282
DB 415 GGTGGSSSPNDPVT-----NIGQAARKQFTVWMAKIPHESSSLFDVRLLESQW 368
UY 283 MEVIMMOLMRSIDHCKIIFAPDVIIDPEKCVGHELEPDMILA-TTSPEPELKH 341
DB 369 NELLIASFSRSDIVPGCHILALGIVHNSASHA-GVGAIPDVI TELVSKMIPMBIK 427
UY 342 KEVLYKAMILLNSSMYPVTAIGVQALSSKRLAHINAVITAIWVIAVIAKSGISSQOSMR 401
DB 428 TELGCRALILFMDPAKGL-----SNPSEVEVLREKVASLETYCKOKYPPDOG--K 477
UY 402 LANIMLISHVRHASKRMCHILNMCKRVVVPYDILLEMNA 444
DB 478 FAKILLRLPALRSIGLKEHLPEFKLIGDTPIDITLMEMLFA 520

RESULT 34

US-07-952-800-2
Sequence 2, Application US/07952800
Patent No. 540925
GENERAL INFORMATION:
APPLICANT: OZATO, KEIKO
TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND AND TOWNSEND
STREET: 1 MARKET PLAZA, STEWART TOWER, SUITE 2000
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
RELION TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 1997-05-28
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE TO PREVIOUS APPLICATION: 15280-21-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
TOPOLOGY: Inout
MOLECULE TYPE: protein
US 97 952-800-2

Query Match 18.2% Score 458.5; DB 1; Length 533;
Best Local Similarity 30.2%; Pred. No. 5,9e-41;
Matches 140; Conservative 63; Mismatches 163; Indels 97; Gaps 17;

UY 9 VTINLEGPBQHTSPNVIWPTPCHISPLVHPQLSHLVAPKSPWCEASLEHILPVN- 67
DB 136 ISSMSGSPGPPAP-----PG-----FSGVSSPDINSTV---SLPGG 172
UY 68 KEIKKRVSSNR CASPVIGSKRIAHAVAVSGVAGVYVWMSPPCKAFK 121

173 SGPPEVKKPVIVAGVIGLITPPPGGCGACK--HICZALICDURSSKRIKIVYSGHAKGKGRK 240
 172 PSTGIMVYGVATNPGTTTOKNPKSGVAFKPKYEVGVNPGSPPEPVIVPKGKES 181
 171 KTIKRIKLYSRKRNKCTVDRKQBNPGVYFVAKKILATYMKRPVAVGK-----KQPG 282
 162 ALDGLHACKAKFSCHAPVPELLELALSTPEALVLLLEAFAPVIL----- 279
 161 KIKD-----GPGVAGG-----APHEMVDRILFAN--LAVKQSGGCVGK 422
 160 240 SPSAFPTASMMMSLTKLADKELVIMSWAKTGVNLSSTLVGVLKESW 282
 159 423 GGVGSSSSNDPVY-----NIGVADKQLEFVYMAKRIPIRSTPLIDGVILLKAW 476
 158 MEVIMMIMMPSLEHPSKLEFADIVLPGVGVVLTLELMLA-LTSPPLKQD 441
 157 NEILLASPSRSTIVKRIKILATGVHNSAUSA-GVADTIDKVLLEVSMDKMDIK 445
 156 442 KETLVKAMILLNSMPTVATQVADSSKRLAHINATVDAVWYIAKSSISGQSGR 401
 155 446 TELGTRALITFENKAKL-----SNESEVEILKERVYASLEFYCKKYPGCG 485
 154 402 LANLMLSHVHASKGMELIMKCKVNVVYDILLMLNA 444
 153 486 FAKLIRPAPRISGKICERHLEFKLIGTIDITMLMKA 528

RESULT 45
 US 07 952 800-4
 Sequence 4: Application US/07952800
 Patent No. 5403925

GENERAL INFORMATION:
 APPLICANT: OZAKI, KEIKO
 TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMONE
 RECEPTOR SUPERFAMILY AND A DNA CLONE THEREOF
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSEND AND TOWNSEND
 STREET: 1 MARKET PLAZA, STEWARD TOWER, SUITE 2000
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/952,800
 FILING DATE: 19920928
 CLASSIFICATION: 445
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 41,677
 REFERENCE/EXCISE NUMBER: 15,280 21 1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415 544-9609
 TELEFAX: 415 544 5044
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DIS 07 952 800 4

Query Match 18.1% Score 459.5; DB 1; Length 446;
 Post Local Similarity 40.2%; Pred. No. 9,40-41;
 Matches 140; Conservative 62; Mismatches 164; Indels 97; Gaps 17;
 9 VTNIKGGKQTTSPNVIWIPGHSIVVHROLSHIYAFKQSKWFAKRSLEHTLPPV 67

110 49 LSSMSKSPGLPVAV-----KQ-----FSGVSSIQDINIV--SLPAGG 85
 97 48 PETIKKVSRR--CAVYVGGSKRIAHFVAVSDVASYHYVSWSTGKAKK 121
 106 86 SGPPEVKKPVIVAGVIGLITPPPGGCGACK-PIVAVIPSSKRIKIVYSGHAKGKGRK 143
 97 122 KTIKRIKLYSRKRNKCTVDRKQBNPGVYFVAKKILATYMKRPVAVGK-----KQPG 181
 106 144 KTIKRIKLYSRKRNKCTVDRKQBNPGVYFVAKKILATYMKRPVAVGK-----KQPG 195
 97 182 ALDGLHACKAKFSCHAPVPELLELALSTPEALVLLLEAFAPVIL----- 229
 106 196 KIKD-----GPGVAGG-----APHEMVDRILFAN--LAVKQSGGCVGK 235
 97 240 SPSAFPTASMMMSLTKLADKELVIMSWAKTGVNLSSTLVGVLKESW 282
 106 246 GGVGSSSSNDPVY-----NIGVADKQLEFVYMAKRIPIRSTPLIDGVILLKAW 289
 97 284 MEVIMMIMMPSLEHPSKLEFADIVLPGVGVVLTLELMLA-LTSPPLKQD 441
 106 290 NEILLASPSRSTIVKRIKILATGVHNSAUSA-GVADTIDKVLLEVSMDKMDIK 448
 97 442 KETLVKAMILLNSMPTVATQVADSSKRLAHINATVDAVWYIAKSSISGQSGR 401
 106 446 TELGTRALITFENKAKL-----SNESEVEILKERVYASLEFYCKKYPGCG 486
 97 402 LANLMLSHVHASKGMELIMKCKVNVVYDILLMLNA 444
 106 486 FAKLIRPAPRISGKICERHLEFKLIGTIDITMLMKA 441

RESULT 46
 5224606-6
 Patent No. 5224606
 APPLICANT: BLAUDIN DE THE, HUGHES, MARC LO, AGNES, TROJANS,
 PIERRE-DEJEAN, ANNE

TITLE OF INVENTION: STEROID/HYROID HORMONE RECEPTOR-RELATED
 PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/134,130
 FILING DATE: 17-DEC-1987
 PRIOR APPLICATION DATA:
 SEQ ID NO: 63
 LENGTH: 463
 5224606-6

Query Match 17.9% Score 451; DB 6; Length 463;
 Post Local Similarity 32.4%; Pred. No. 2,1e-40;
 Matches 105; Conservative 64; Mismatches 125; Indels 30; Gaps 10;

97 96 GAVSDVASYHYGVWSTEDTKAFKRSIQDINIVGVAVNGTTIDKRNKSGCAKRLK 155
 106 1 CLOGDEASGCHVGLGSGKVFRRKMGQINYLAVGRNCTVDRKRNTPAKRQK 60
 97 156 GYVWNGVEGGRLEKSYKELVHNSAUSA-GVADTIDKVLLEVSMDKMDIK 214
 106 61 GGVGSSVLAGRKKK--FNKRVKALD-----AVALLAVGLTMSQK--LSTPQK 110
 97 215 ---VLTLEAFPPVVLSPESA-PTFASMMMSLTKLADKELVIMSWAKTSPV 257
 106 111 IGLIPPLIMSLPGVATVAGGNRIPIRSTPLIDGVILLKAW 170
 97 268 ELSTFVGVLLSSWQVIMMIMMPSLEHPSKLEFADIVLPGVGVVLTLELMLA-LTSPPLKQD 425
 106 171 NEILLASPSRSTIVKRIKILATGVHNSAUSA-GVADTIDKVLLEVSMDKMDIK 448
 97 426 MEVIMMIMMPSLEHPSKLEFADIVLPGVGVVLTLELMLA-LTSPPLKQD 441
 106 442 KETLVKAMILLNSMPTVATQVADSSKRLAHINATVDAVWYIAKSSISGQSGR 401
 97 486 VVIA--KSGISSGQSGRIANLL 406

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 15, 2003, 13:15:19 ; Search time 51.9571 seconds
(without alignments)
981,555 Million cell updates/sec

Title: US-08-826-361a-5

Project source: 2522

Sequence: 1 MMYSTPSNNVNLSPGPGPGT PGPVANSYSPVNSVNPST 477

Scoring table:

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Searched: 408643 seqs, 125915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications-AA:
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14: /cgn2_6/prodat/a/2/pubppaa/us06_PDB_PDP_*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1202	47.4	595	9
4	1195	47.4	595	9
5	1195	47.4	595	9
6	1195	47.4	595	9
7	1195	47.4	595	9
8	1195	47.4	595	9
9	1195	47.4	595	9
10	1195	47.4	595	9
11	1193	47.3	595	9
12	1192	47.3	595	9
13	1190	47.2	595	9
14	1145	45.4	701	9
15	1145	45.4	701	9
16	958.5	38.0	1099	9
17	920	35.5	1147	9
18	814.5	32.3	910	9
19	814.5	32.3	922	9

20	770	40.5	422	10	US-09-747-255-5	Sequence 5, App1
21	768	40.5	241	10	US-09-905-176-14	Sequence 14, App1
22	763	40.3	547	9	US-10-052-092-10	Sequence 10, App1
23	763	40.3	660	10	US-09-853-083-4	Sequence 4, App1
24	762	40.2	243	10	US-09-903-876-1	Sequence 1, App1
25	760	40.1	660	10	US-09-853-083-8	Sequence 8, App1
26	751	39.8	660	10	US-09-853-083-6	Sequence 6, App1
27	746.5	39.6	264	9	US-1-144-583-1	Sequence 1, App1
28	745.5	39.6	264	9	US-09-885-827-2	Sequence 2, App1
29	741.5	38.5	519	9	US-10-211-239-1	Sequence 1, App1
30	504	20.0	99	10	US-09-864-761-48783	Sequence 48783, A
31	460.5	18.3	689	9	US-10-202-826-2	Sequence 2, App1
32	459.5	18.2	532	9	US-09-922-226-2	Sequence 2, App1
33	459.5	18.2	532	9	US-10-098-184-2	Sequence 2, App1
34	440	17.4	463	9	US-09-922-226-3	Sequence 3, App1
35	440	17.4	463	9	US-10-098-184-3	Sequence 3, App1
36	434.5	17.2	462	9	US-09-922-226-1	Sequence 1, App1
37	434.5	17.2	462	9	US-10-098-184-1	Sequence 1, App1
38	434	17.2	462	10	US-09-965-703-6	Sequence 6, App1
39	434	17.2	777	9	US-10-153-668-226	Sequence 226, App1
40	432.5	17.1	472	10	US-09-965-703-61	Sequence 61, App1
41	428.5	17.0	598	9	US-10-211-239-2	Sequence 2, App1
42	428.5	17.0	598	10	US-09-853-386-91	Sequence 91, App1
43	428.5	17.0	598	10	US-09-853-386-98	Sequence 98, App1
44	425.5	16.9	597	10	US-09-853-386-93	Sequence 93, App1
45	425.5	16.9	907	9	US-10-008-239-2	Sequence 2, App1
46	424.5	16.8	1070	9	US-10-001-4868-2	Sequence 2, App1
47	422.5	16.8	988	9	US-09-997-267-2	Sequence 2, App1
48	422.5	16.8	294	9	US-09-997-267-4	Sequence 4, App1
49	421	16.7	601	10	US-09-853-386-92	Sequence 92, App1
50	421	16.7	601	10	US-09-853-386-94	Sequence 94, App1
51	420	16.7	598	10	US-09-853-386-91	Sequence 91, App1
52	419	16.6	460	9	US-09-965-703-6	Sequence 6, App1
53	419	16.6	460	9	US-10-295-370-4	Sequence 4, App1
54	416.5	16.5	466	9	US-09-909-556-2	Sequence 2, App1
55	416.5	16.5	477	10	US-09-853-386-42	Sequence 42, App1
56	416.5	16.5	598	10	US-09-853-386-94	Sequence 94, App1
57	416.5	16.5	598	10	US-09-853-386-93	Sequence 93, App1
58	416.5	16.5	598	10	US-09-853-386-37	Sequence 37, App1
59	416.5	16.5	598	10	US-09-853-386-38	Sequence 38, App1
60	416.5	16.5	598	10	US-09-853-386-39	Sequence 39, App1
61	416.5	16.5	598	10	US-09-853-386-40	Sequence 40, App1
62	416.5	16.5	598	10	US-09-853-386-41	Sequence 41, App1
63	416.5	16.5	598	10	US-09-853-386-45	Sequence 45, App1
64	416.5	16.5	598	10	US-09-853-386-35	Sequence 35, App1
65	416.5	16.5	598	10	US-09-853-386-36	Sequence 36, App1
66	416.5	16.5	598	10	US-09-853-386-45	Sequence 45, App1
67	385	15.3	643	10	US-09-853-386-95	Sequence 95, App1
68	385	15.3	597	10	US-09-853-386-97	Sequence 97, App1
69	381	15.1	73	9	US-09-879-746-1	Sequence 67, App1
70	378	15.0	627	10	US-09-853-386-67	Sequence 67, App1
71	378	15.0	627	10	US-10-095-169-2	Sequence 2, App1
72	378	15.0	628	10	US-09-853-386-66	Sequence 66, App1
73	377	14.9	628	10	US-09-853-386-66	Sequence 66, App1
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90	372	14.9	628	10	US-09-853-386-66	Sequence 66, App1
91	372	14.9	628	10	US-09-853-386-66	Sequence 66, App1
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[illegible]

CHICKEN

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NUMBER_OF_SEQ_ID NOS: 14
SOFTWARE: PATENT Vot. 2.1
SEQ_ID No: 2
LENGTH: 505
TYPE: FRF
ORGANISM: Homo sapiens
DS: 09-054-044-2

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385 WVAJAKSGTGGGQSMWANIIMLSHVHAKSGMEHLLNKKCNVVPVYDLEMLNA 444
487 IHMAKAGTIGQOHQALQALILSHIRMSKMEHLYSMKCNVVPVYDLEMLNA 546
445 HVL 447
547 HVL 549

RESULT 4
US-10-052-092-40
Sequence 30, Application US/10052092
Publication No. US2003002777A1
GENERAL INFORMATION:
APPLICANT: Fougna, Suzanne
APPLICANT: Alfred, D.
APPLICANT: Hopp, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapies
FILE REFERENCE: P02102052
CURRENT APPLICATION NUMBER: US/10/052,092
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: us 60/242,990
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/304,018
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent In version 4.1
SEQ ID NO 30
LENGTH: 595
TYPE: PRI
ORGANISM: hamster
US-10-052-092-40

Query Match 47.7% Score 1297 DB 9 Length 595
Best Local Similarity 50.7% Prod. No. 90-99
Matches 246 Conservative 87 Mismatches 122 Indels 30 Gaps 10

16 EGRGTTSTN VIMPTCHSP LVVHRSI SHI YAPPOKSPGTFAPSLFHT FVNFRT 71
97 POLNSVSPSLMLHPPPOLSFELHRLQVPTYLENSAA VHSPPAFYPSN 156
72 KKKVGNRCASPVGTGSK RDAHFAVGSQVAVHGVNSGCKAKAFKST 126
156 NKRSGFPRFSSSFKSGMAMFVKEFPYCAVNPVAVSYHATVWSEFKAFKST 215
127 HNYTPATVGTTRKPKKSKQVTPRPVYVWVWVGVSPRPVYVYVFPKST 194
215 HNDVMTATVQCTTKPKKSKQVTPRPVYVWVWVGVSPRPVYVYVFPKST 215
185 --GIFACAKPST --GHAFFVELLDALSPQVLTLEKPBVLT 272
276 GNNIMGSGMRAINIWPSPVLRKTKKNSPALSLTDQVMSALLMEPLTYSEYR 433
233 SAFTTASMMGLTKLAKELVHMSAKKIPGFVLSLQVRLLESQWVLMGIMM 292
434 SRPSEASMMGLTINLAFETVHIMINAKKVPGEFENHQQVHIFVAMI 493
293 KSTHPRKITEAPFVTPRPGVVFETIFIFMLATTSPEFETKTEFTLVANML 452
494 KSMHPRKITEAPFVTPRPGVVFETIFIFMLATTSPEFETKTEFTLVANML 453
453 LNSMPLVATQDAUSPKIANTNAVTVALWVAJAKSGTGGGQSMWANIIMLSHV 411
454 LNSGVYTFELSTKSLFEKDIHVLDEKTDVTLHMAVAGLTLQVGHRLAELLISH 513
412 VHAASNGMEHLLNKKCNVVPVYDLEMLNAHVI 471
514 IHMSNGMEHLLNKKCNVVPVYDLEMLNAHRL--TPVSRMGVSPSEPSQLTT 570
472 UNPOS 476
571 INSTS 575

385 WVAJAKSGTGGGQSMWANIIMLSHVHAKSGMEHLLNKKCNVVPVYDLEMLNA 444
487 IHMAKAGTIGQOHQALQALILSHIRMSKMEHLYSMKCNVVPVYDLEMLNA 546
445 HVL 447
547 HVL 549

RESULT 4
US-10-096-710-1
Sequence 1, Application US/10096710
Patent No. US20020164581A1
GENERAL INFORMATION:
APPLICANT: Chang, Chawshang
TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: DO NOT ATTENUATE THE PROTECTIVE EFFECTS OF BSKOGEN
FILE REFERENCE: 21108,001002
CURRENT APPLICATION NUMBER: US/10/096,710
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/275,229
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 595
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: FastSeq for Windows Version 4.0
US-10-096-710-1

Query Match 47.4% Score 1195 DB 9 Length 595
Best Local Similarity 50.7% Prod. No. 80-98
Matches 245 Conservative 81 Mismatches 103 Indels 54 Gaps 10

10 TNEGGGPGP-----TTPSVLWPTGHSPI LVVHRSI SHI YAPPOK 50
76 TGLPYGGSFRAAFSGMGLGPPPLNSVSPSLMLHPPPOLSFELHRLQVPTYLE 135
51 KSIWCFANSEHTITVNEETIKFVSCN--ASVPLTQ--SKPLAHFAVSDVA 103
136 ESTVTEAASHPAYVPS--NSINHGQSGTFPLASINHGMAAMSAKELVAVNPVA 192
104 SCYHGVWSP--KAFKPSLQGNIVYVATNQCITLIPKPSQVWCTLPKCYFVGVK 163
193 SHAVVWSP--KAFKPSLQGNIVYVATNQCITLIPKPSQVWCTLPKCYFVGVK 252
164 GNSPFPVYVLPVPSAPFQI--ATKAPKSTHAPVY-----ETIT 207
253 GQPKQDPMQIMTKWQDPR-----QPDGCVSGGCMRAAMKQSPMTKSPFV 407
208 DASTSEGVLLLEFATHVLSR--SAFTTASMMGLTKLAKELVHMSAKKIPG 265
408 GELTADVMSALLAEFT--TASDALT--KPFSSAMKTLINCAI 464
266 FVRSSTDOVWLESQWMEFVLMGLHWEGTDHMKLIFAPDVLDHRSKGVGGLTET 425
467 FVDTLHDQVHLEFCAMETIMCTIVWRSRHHVKILFANLILIDNQGKCVHMYETD 426
426 MLATTSFRKLIKHEVLCVAMTILNSMVEVATQDAUSPKIANTNAVTVAL 484
427 MLATTSFRKLIKHEVLCVAMTILNSMVEVATQDAUSPKIANTNAVTVAL 484
485 WVAJAKSGTGGGQSMWANIIMLSHVHAKSGMEHLLNKKCNVVPVYDLEMLNA 444
487 IHMAKAGTIGQOHQALQALILSHIRMSKMEHLYSMKCNVVPVYDLEMLNA 546
445 HVL 447
547 HVL 549

RESULT 5
US-10-081-563-2
Sequence 2, Application US/10081563
Publication No. US20020187496A1
GENERAL INFORMATION:
APPLICANT: Wake Forest University

ORGANISM: human
US-10-052-092-13

Query Match 47.4% Score 1195; DB 9; Length 595;
Best Local Similarity 50.7% Pred. No. 3, Re-98,
Matches 245; Conservative 81; Mismatches 103; Indels 54; Gaps 10;

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QY 10 TNLGGGGRG-----TSPNVIWPTGGHSP-LVHKGQLSHYATG 50
DB 76 TGLVYGGSEAAAGSGMGLAGPPPLNSVSPSLMLLHPPOLSPTGLPBGQVYYLENE 135
QY 51 KSPWC-FASLEHTLVNFTTKRVSNGRCASEVTSQ-----SRGAAHCAVCSQYA 103
DB 136 PSQYVFEAGPPAPYR-----NSNRGQGRERLASTNDGSMAMSAKETRCAVCAVNYA 192
QY 104 SGHYVWVSGCEGKAFKRSIGCHNYGTPATNGTIDRNRKSGVAFKCYGVGMK 163
DB 193 SGHYVWVSGCEGKAFKRSIGCHNYGTPATNGTIDRNRKSGVAFKCYGVGMK 252
QY 164 GCSPPRGCGYPIVPPGASAPGQHFCAGKAKRSGGHPYV-----P11 207
DB 253 GGTTRKPRGGRMFKRKGPRD-----GEGGEGVSGGMPPAANIWSPPLMTRSKNSLA 307
QY 208 DALSPQGLVTLLEAPPHVLSR--PSAPFEASMMKSLTKLACEVYHMSMAKIDG 265
DB 408 LSTADQMVASALLDAEP-ILYSYDPTRFPSASMMGLITNADRELVHMINMAKRVG 366
QY 266 FVELSLDQVLLSEVMKELMMKRLSDHDKLIPAPVYIDRERKCYEGTLEFD 425
DB 467 FVDLIDQVLLSEVMKELMMKRLSDHDKLIPAPVYIDRERKCYEGTLEFD 426
QY 426 MLATSRPEFLKQHEFYGVKAMILLNSMPTVAT-GRADSRKLAHLINAVTAL 484
DB 427 MLATSRPEFLKQHEFYGVKAMILLNSMPTVAT-GRADSRKLAHLINAVTAL 486
QY 485 VVVIKSGJSSQGSMSPLANLMLSHVPSNRKGMELNMKKNVAVYDLEMLNA 444
DB 487 IELMAKAGLTQQOHQRLAQILILSHIRMSKMKMHLYSMCKKNVAVYDLEMLNA 546
QY 445 HVL 447
DB 547 HRL 549

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RESULT 8

US-10-052-092-14

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? Sequence 14, Application US/10052092
? Publication No. US2003002778A1
? GENERAL INFORMATION:
? APPLICANT: Fujita, Suzanne
? APPLICANT: Alfred, D.
? APPLICANT: Hopp, Torsten A.
? APPLICANT: O'Connell, Peter
? TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapies
? FILE REFERENCE: P02102052
? CURRENT APPLICATION NUMBER: US/10/052-092
? PRIOR FILING DATE: 2002-01-18
? PRIOR APPLICATION NUMBER: US 60/292,990
? PRIOR FILING DATE: 2001-01-19
? PRIOR APPLICATION NUMBER: US 60/404,018
? PRIOR FILING DATE: 2001-07-09
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: Patent In version 3.1
? SEQ ID NO 14
? LENGTH: 595
? TYPE: PRT
? ORGANISM: Human
US-10-052-092-14

```

Query Match 47.4% Score 1195; DB 9; Length 595;
Best Local Similarity 50.7% Pred. No. 3, Re-98;
Matches 245; Conservative 81; Mismatches 103; Indels 54; Gaps 10;

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QY 10 TNLGGGGRG-----TSPNVIWPTGGHSP-LVHKGQLSHYATG 50
DB 76 TGLVYGGSEAAAGSGMGLAGPPPLNSVSPSLMLLHPPOLSPTGLPBGQVYYLENE 135
QY 51 KSPWC-FASLEHTLVNFTTKRVSNGRCASEVTSQ-----SRGAAHCAVCSQYA 103
DB 136 PSQYVFEAGPPAPYR-----NSNRGQGRERLASTNDGSMAMSAKETRCAVCAVNYA 192
QY 104 SGHYVWVSGCEGKAFKRSIGCHNYGTPATNGTIDRNRKSGVAFKCYGVGMK 163
DB 193 SGHYVWVSGCEGKAFKRSIGCHNYGTPATNGTIDRNRKSGVAFKCYGVGMK 252
QY 164 GCSPPRGCGYPIVPPGASAPGQHFCAGKAKRSGGHPYV-----P11 207
DB 253 GGTTRKPRGGRMFKRKGPRD-----GEGGEGVSGGMPPAANIWSPPLMTRSKNSLA 307
QY 208 DALSPQGLVTLLEAPPHVLSR--PSAPFEASMMKSLTKLACEVYHMSMAKIDG 265
DB 408 LSTADQMVASALLDAEP-ILYSYDPTRFPSASMMGLITNADRELVHMINMAKRVG 366
QY 266 FVELSLDQVLLSEVMKELMMKRLSDHDKLIPAPVYIDRERKCYEGTLEFD 425
DB 467 FVDLIDQVLLSEVMKELMMKRLSDHDKLIPAPVYIDRERKCYEGTLEFD 426
QY 426 MLATSRPEFLKQHEFYGVKAMILLNSMPTVAT-GRADSRKLAHLINAVTAL 484
DB 427 MLATSRPEFLKQHEFYGVKAMILLNSMPTVAT-GRADSRKLAHLINAVTAL 486
QY 485 VVVIKSGJSSQGSMSPLANLMLSHVPSNRKGMELNMKKNVAVYDLEMLNA 444
DB 487 IELMAKAGLTQQOHQRLAQILILSHIRMSKMKMHLYSMCKKNVAVYDLEMLNA 546
QY 445 HVL 447
DB 547 HRL 549

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RESULT 9

US-09-952-680A-10

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? Sequence 10, Application US/09052680A
? Publication No. US2003008739A1
? GENERAL INFORMATION:
? APPLICANT: Stanton, Mary
? APPLICANT: Epstein, David
? APPLICANT: Hamaguchi, No. US2003008739A1uko
? TITLE OF INVENTION: Target Activated Biosensor and Methods of Using Same
? FILE REFERENCE: 23239-501
? CURRENT APPLICATION NUMBER: US/09/952-680A
? PRIOR FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: 60/232,454
? PRIOR FILING DATE: 2000-09-14
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 10
? LENGTH: 595
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-952-680A-10

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Query Match 47.4% Score 1195; DB 9; Length 595;
Best Local Similarity 50.7% Pred. No. 3, Re-98;
Matches 245; Conservative 81; Mismatches 103; Indels 54; Gaps 10;

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QY 10 TNLGGGGRG-----TSPNVIWPTGGHSP-LVHKGQLSHYATG 50
DB 76 TGLVYGGSEAAAGSGMGLAGPPPLNSVSPSLMLLHPPOLSPTGLPBGQVYYLENE 135
QY 51 KSPWC-FASLEHTLVNFTTKRVSNGRCASEVTSQ-----SRGAAHCAVCSQYA 103
DB 136 PSQYVFEAGPPAPYR-----NSNRGQGRERLASTNDGSMAMSAKETRCAVCAVNYA 192
QY 104 SGHYVWVSGCEGKAFKRSIGCHNYGTPATNGTIDRNRKSGVAFKCYGVGMK 163
DB 193 SGHYVWVSGCEGKAFKRSIGCHNYGTPATNGTIDRNRKSGVAFKCYGVGMK 252
QY 164 GCSPPRGCGYPIVPPGASAPGQHFCAGKAKRSGGHPYV-----P11 207
DB 253 GGTTRKPRGGRMFKRKGPRD-----GEGGEGVSGGMPPAANIWSPPLMTRSKNSLA 307
QY 208 DALSPQGLVTLLEAPPHVLSR--PSAPFEASMMKSLTKLACEVYHMSMAKIDG 265
DB 408 LSTADQMVASALLDAEP-ILYSYDPTRFPSASMMGLITNADRELVHMINMAKRVG 366
QY 266 FVELSLDQVLLSEVMKELMMKRLSDHDKLIPAPVYIDRERKCYEGTLEFD 425
DB 467 FVDLIDQVLLSEVMKELMMKRLSDHDKLIPAPVYIDRERKCYEGTLEFD 426
QY 426 MLATSRPEFLKQHEFYGVKAMILLNSMPTVAT-GRADSRKLAHLINAVTAL 484
DB 427 MLATSRPEFLKQHEFYGVKAMILLNSMPTVAT-GRADSRKLAHLINAVTAL 486
QY 485 VVVIKSGJSSQGSMSPLANLMLSHVPSNRKGMELNMKKNVAVYDLEMLNA 444
DB 487 IELMAKAGLTQQOHQRLAQILILSHIRMSKMKMHLYSMCKKNVAVYDLEMLNA 546
QY 445 HVL 447
DB 547 HRL 549

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1b 193 SCYHYGVWSFEGKAFKESLQCHNDYMTATMCTLDKMKRSYGAATLKKYEVWMMK 252
1b 164 GCSRRRGYRYLVYRORSADPOLHFCARAKRSRGAHVR ----- ELL 207
1b 253 GGIKKRKRGGKMLKIRKRDND ----- GIKRRCVYSAAMKRAANLMTSLMLKRSKKNLA 407
1b 208 IATSPGCVLTLEAPPHVILSR -PSAPFTASMMNSTKLADRELVMISWARK193 245
1b 408 LSTLADQMSALLDAEPP-LIYSEYDPTRESEASMMGLTINLADRELVMIMWARKV93 466
1b 266 FVELSLFDQVRLLESYWMYVIMMGIMKRSIDHCKRLFAVDLVADKRCVAGSLLEFD 425
1b 467 FVDLTLDQVRLLECAWLELIMGLVWSMSMEHVKLEAPNLLDRNGKVESEVLEFD 426
1b 426 MLATTSRRELKIDREYLVKAMILLNSSMYPLVAT-QDASSRKLAILNAVTDAL 484
1b 427 MLATTSRFRMMNIGREYVGLKSLILNSGYFTLSSTLKSLFEKHIDHVDKTDITL 486
1b 485 VVVIARSGTSSQOOSRILANLMLSLVHASKKGMHEILNKKRNVVYVILLLEMLNA 444
1b 487 IHIMAKKATLQOQHRLAQLLLLSHRIMSKKGMHEILYSMKCKNVVYVILLLEMLDA 546
1b 445 HVL 447
1b 547 HVL 549

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RESULT 10
US 09 943 267A 2
Sequence 2, Application US/09943267A
Publication No. US20020124095A1
GENERAL INFORMATION:
APPLICANT: Kalush, Francis et al.
TITLE OF INVENTION: Estrogen receptor alpha variants and
FILE REFERENCE: CLO00258C14
CURRENT APPLICATION NUMBER: US/09/943,267A
PRIOR FILING DATE: 2001-04-21
PRIOR APPLICATION NUMBER: 60/160626
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 60/184756
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 09/692414
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/768184
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 09/804076
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 09/826314
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 595
TYPE: PRT
ORGANISM: HUMAN
US 09 943 267A 2

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Query Match 47.4% Score 1195 DB 10 Length 595
Host Local Similarity 50.7% Prod. No. 3,86-98
Matches 2493 Conservative 81 Mismatches 103 Indels 54 Gaps 10
1b 10 INFERGRO -----TTSNVLMTTGHSL-LVHQLSHLYAEQ 50
1b 76 SGLAVGDSBAAPANLGPPLNVSFSLVLIHPPVLSPELHBRQVYVYLENE 145
1b 51 KSWP-EARSEHTLPVNRETLKKRVSNRCASPTGPG-----SKRIAHFVAVSYVA 104
1b 136 PSYTVAFAGVAFYFP-NSDNRGCGREKLASIDKSGMAMESAKETRYCAVNDVA 192
1b 193 SCYHYGVWSFEGKAFKESLQCHNDYMTATMCTLDKMKRSYGAATLKKYEVWMMK 252
1b 208 IATSPGCVLTLEAPPHVILSR -PSAPFTASMMNSTKLADRELVMISWARK1 245
1b 408 LSTLADQMSALLDAEPP-LIYSEYDPTRESEASMMGLTINLADRELVMIMWARKV 466
1b 266 FVELSLFDQVRLLESYWMYVIMMGIMKRSIDHCKRLFAVDLVADKRCVAGSLLEFD 425
1b 467 FVDLTLDQVRLLECAWLELIMGLVWSMSMEHVKLEAPNLLDRNGKVESEVLEFD 426
1b 426 MLATTSRRELKIDREYLVKAMILLNSSMYPLVAT-QDASSRKLAILNAVTDAL 484
1b 427 MLATTSRFRMMNIGREYVGLKSLILNSGYFTLSSTLKSLFEKHIDHVDKTDITL 486
1b 485 VVVIARSGTSSQOOSRILANLMLSLVHASKKGMHEILNKKRNVVYVILLLEMLNA 444
1b 487 IHIMAKKATLQOQHRLAQLLLLSHRIMSKKGMHEILYSMKCKNVVYVILLLEMLDA 546
1b 445 HVL 447
1b 547 HVL 549

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1b 164 GCSRRRGYRYLVYRORSADPOLHFCARAKRSRGAHVR ----- ELL 207
1b 253 GGIKKRKRGGKMLKIRKRDND ----- GIKRRCVYSAAMKRAANLMTSLMLKRSKKNLA 407
1b 208 IATSPGCVLTLEAPPHVILSR -PSAPFTASMMNSTKLADRELVMISWARK193 245
1b 408 LSTLADQMSALLDAEPP-LIYSEYDPTRESEASMMGLTINLADRELVMIMWARKV93 466
1b 266 FVELSLFDQVRLLESYWMYVIMMGIMKRSIDHCKRLFAVDLVADKRCVAGSLLEFD 425
1b 467 FVDLTLDQVRLLECAWLELIMGLVWSMSMEHVKLEAPNLLDRNGKVESEVLEFD 426
1b 426 MLATTSRRELKIDREYLVKAMILLNSSMYPLVAT-QDASSRKLAILNAVTDAL 484
1b 427 MLATTSRFRMMNIGREYVGLKSLILNSGYFTLSSTLKSLFEKHIDHVDKTDITL 486
1b 485 VVVIARSGTSSQOOSRILANLMLSLVHASKKGMHEILNKKRNVVYVILLLEMLNA 444
1b 487 IHIMAKKATLQOQHRLAQLLLLSHRIMSKKGMHEILYSMKCKNVVYVILLLEMLDA 546
1b 445 HVL 447
1b 547 HVL 549

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RESULT 11
US 10 052 092-31
Sequence 31, Application US/10052092
Publication No. US20030027778A1
GENERAL INFORMATION:
APPLICANT: Fuqua, Suzanne
APPLICANT: Allrod, D.
APPLICANT: Hopp, Kristen A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapy
FILE REFERENCE: P021020S2
CURRENT APPLICATION NUMBER: US/10/052,092
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,990
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/404,018
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent In Version 3.1
SEQ ID NO: 31
LENGTH: 595
TYPE: PRT
ORGANISM: HUMAN
US 10 052 092-31

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Query Match 47.3% Score 1194 DB 9 Length 595
Host Local Similarity 49.1% Prod. No. 5,76-98
Matches 2493 Conservative 86 Mismatches 110 Indels 62 Gaps 14
1b 10 INFERGRO -----TTSNVLMTTGHSL-LVHQLSHLYAEQ 50
1b 76 SGLAVGDSBAAPANLGPPLNVSFSLVLIHPPVLSPELHBRQVYVYLENE 145
1b 51 KSWP-EARSEHTLPVNRETLKKRVSNRCASPTGPG-----SKRIAHFVAVSYVA 104
1b 136 PSYTVAFAGVAFYFP-NSDNRGCGREKLASIDKSGMAMESAKETRYCAVNDVA 192
1b 193 SCYHYGVWSFEGKAFKESLQCHNDYMTATMCTLDKMKRSYGAATLKKYEVWMMK 252
1b 208 IATSPGCVLTLEAPPHVILSR -PSAPFTASMMNSTKLADRELVMISWARK1 245
1b 408 LSTLADQMSALLDAEPP-LIYSEYDPTRESEASMMGLTINLADRELVMIMWARKV 466
1b 266 FVELSLFDQVRLLESYWMYVIMMGIMKRSIDHCKRLFAVDLVADKRCVAGSLLEFD 425
1b 467 FVDLTLDQVRLLECAWLELIMGLVWSMSMEHVKLEAPNLLDRNGKVESEVLEFD 426
1b 426 MLATTSRRELKIDREYLVKAMILLNSSMYPLVAT-QDASSRKLAILNAVTDAL 484
1b 427 MLATTSRFRMMNIGREYVGLKSLILNSGYFTLSSTLKSLFEKHIDHVDKTDITL 486
1b 485 VVVIARSGTSSQOOSRILANLMLSLVHASKKGMHEILNKKRNVVYVILLLEMLNA 444
1b 487 IHIMAKKATLQOQHRLAQLLLLSHRIMSKKGMHEILYSMKCKNVVYVILLLEMLDA 546
1b 445 HVL 447
1b 547 HVL 549

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Best Local Similarity 49.2%; Pred. No. 1.2e-76;
Matches 190; Conservative 71; Mismatches 92;
Indels 33; Gaps 6

Matches 190; conservative 71; mismatches 92; indels 33; gaps 6

[illegible]

RESULT 17
US-10-259-864-1

```

1 Publication No. US20030077645A1
2 GENERAL INFORMATION:
3 APPLICANT: Hager, Gordon L.
4 TITLE OF INVENTION: Superficially Pore-fused Chimera's, Anticancer Assay For
5 TITLE OF INVENTION: Receptor Ligands, and Methods and Kits for Detecting a
6 TITLE OF INVENTION: Ligands
7 FILE REFERENCE: 24799
8 CURRENT APPLICATION NUMBER: US/10/259,864
9 CURRENT FILING DATE: 2002-09-30
10 PRIOR APPLICATION NUMBER: US 60/425,178
11 PRIOR FILING DATE: 2001-09-28
12 NUMBER OF SEQ ID NOS: 6
13 SOFTWARE: Patent In version 3.1
14 SEQ ID NO: 1
15 LENGTH: 1147
16 TYPE: PRT
17 ORGANISM: rat/human chimera
18 FEATURE:
19 NAME/KEY: mat_peptide
20 LOCATION: (1..6)
21 OTHER INFORMATION: Chimeric Protein
22 US-10 259 864 1
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1 RESULT 18
2 US-09-908-153B-40
3 Sequence 40, Application US/09908153B
4 Patent No. US202016871A1
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Barbas, Carlos F.
9 APPLICANT: Barbas, Robert
10 APPLICANT: Schopfer, Ulrich
11
12 TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
13 TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
14 TITLE OF INVENTION: SWITCHES
15 FILE REFERENCE: US1 725.1
16 CURRENT APPLICATION NUMBER: US-09/908,153B
17 CURRENT FILING DATE: 2001-07-18
18 PRIOR APPLICATION NUMBER: US 09/619,063
19 PRIOR FILING DATE: 2000-07-18
20 NUMBER OF SEQ ID NOS: 53
21 SOFTWARE: fastsq for windows version 4.0
22 SEQ ID NO 40
23
24 LENGTH: 910
25
26 TYPE: PRT
27
28 ORGANISM: UNKNOWN
29
30 FEATURE:
31
32 OTHER INFORMATION: Synthesized
33
34 US-09-908-153B-40

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[illegible]


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TYPE: PRI
ORGANISM: Homo sapiens
US-09-905-176-14

Query Match
Best Local Similarity 30.58; Score 768; DB 10; Length 241;
Pred Local Similarity 59.8K; Pred No 1 4a-60;
Matches 144; Conservative 56; Mismatches 37; Indels 4; Gaps 4;

QY 210 LSPDQVLTLEAFPHVLSR--PSAPFTASMMMSLTKLAKELVHMSAKKPKPQV 267
DB 1 LTAQOVYSLIDAPRP--IYSEYDPTRPSPASMMGLTNLAPELVHMINNAKRPQV 59
QY 268 FLSFQGVPLTFSSWMPVIMGIMWPSIDHP--KLIFAPPLVILPDQKVEGILPEPML 327
DB 60 DLTIDQVHLLEKAMEFLIMGLVWRSMPHCKLIFAPMLIDPQKVEGQVEIFDML 119
QY 328 LATSPPEPKIQGKPEVLCVAMILLNSMYQVVIAT--QDASSPKLAHLNAVYDALV 386
DB 120 LATSPPEPMNLQEEFVTLKSLILNSVYTFLSSTKSLPEKHILHVLDTITLH 179
QY 387 VIAKSGISSQOOSMRLANLMLLSHVHASNKGHEHLNMKKKNVYVYDILLMLNAH 446
DB 180 LMAKATLIGQGHPLAQIILISHIHMSNKGHEHLNMYCKKNVYVYDILLMLNAH 289
QY 447 L 447
DB 240 L 240

RESULT 22
US-10-052-092-10
Sequence 10; Application US/10052092
Publication No. US2003002778A1
GENERAL INFORMATION:
APPLICANT: Fujita, Suzanne
APPLICANT: Allied, D.
APPLICANT: Bopp, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapies
FILE REFERENCE: P02102982
CURRENT APPLICATION NUMBER: US/10/052,092
CURRENT FILING DATE: 2002-01-19
PRIOR APPLICATION NUMBER: 05 60/262,990
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/304,018
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent version 3.1
SEQ ID NO 10
LENGTH: 547
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthesized. Estimated. Forward direction. Location: 100-100
US-10-052-092-10

Query Match
Best Local Similarity 30.38; Score 763; DB 9; Length 547;
Pred Local Similarity 45.4K; Pred No 1 3a-59;
Matches 164; Conservative 66; Mismatches 83; Indels 48; Gaps 7;

QY 127 HNDYICPATNOCTIDKRRKSCQAGRLKCYEWMKCSRRER-----QGY 173
DB 149 HNYVY-----TADYCKNLIKAKFKIPHNIFDQSVLADHYQNTPIIGAPVILDPNH 201
QY 174 KLVKRSKAPQ-----LHAGKAKSGSHAPVR-----PILLLA 209
DB 202 LSTQSAISKDNRKPRIMVILFFVTAAKMSQSSAGPAPANIWPQGLM--KPYKNSCATS 261
QY 210 LSPDQVLTLEAFPHVLSR--PSAPFTASMMMSLTKLAKELVHMSAKKPKPQV 267
DB 262 LTAQOVYSLIDAPRP--IYSEYDPTRPSPASMMGLTNLAPELVHMINNAKRPQV 320
QY 268 FLSFQGVPLTFSSWMPVIMGIMWPSIDHP--KLIFAPPLVILPDQKVEGILPEPML 327
DB 60 DLTIDQVHLLEKAMEFLIMGLVWRSMPHCKLIFAPMLIDPQKVEGQVEIFDML 119

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QY 421 DLTIDQVHLLEKAMEFLIMGLVWRSMPHCKLIFAPMLIDPQKVEGQVEIFDML 380
DB 328 LATSPPEPKIQGKPEVLCVAMILLNSMYQVVIAT--QDASSPKLAHLNAVYDALV 386
DB 381 LATSPPEPMNLQEEFVTLKSLILNSVYTFLSSTKSLPEKHILHVLDTITLH 440
QY 387 VIAKSGISSQOOSMRLANLMLLSHVHASNKGHEHLNMKKKNVYVYDILLMLNAH 446
DB 441 LMAKATLIGQGHPLAQIILISHIHMSNKGHEHLNMYCKKNVYVYDILLMLNAH 500
QY 447 L 447
DB 501 L 501

RESULT 23
US-09-853-033-4
Sequence 4; Application US/09854034
Patent No. US2002010068A1
GENERAL INFORMATION:
APPLICANT: CHAMBER, PIERRE
APPLICANT: METZGER, DANIEL
TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
FILE REFERENCE: 065601/9222
CURRENT APPLICATION NUMBER: US/09/853,034
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: FR 00/12570
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent ver. 2.1
SEQ ID NO 4
LENGTH: 660
TYPE: PRI
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence; Chamber sequence
US-09-853-033-4

Query Match
Best Local Similarity 30.38; Score 763; DB 10; Length 660;
Pred Local Similarity 59.1K; Pred No 1 7a-59;
Matches 143; Conservative 57; Mismatches 38; Indels 4; Gaps 4;

QY 259 ALSTFLVLTLEAFPHVLSR--PSAPFTASMMMSLTKLAKELVHMSAKKPKPQV 266
DB 374 LTAQOVYSLIDAPRP--IYSEYDPTRPSPASMMGLTNLAPELVHMINNAKRPQV 432
QY 267 VELSLPEVLEESGMEVIMMSTHHPKELIAPRSVIAQSGKGVQDILPEPDM 426
DB 433 VHTIDQVHLLEKAMEFLIMGLVWRSMPHCKLIFAPMLIDPQKVEGQVEIFDML 492
QY 427 LATSPPEPKIQGKPEVLCVAMILLNSMYQVVIAT--QDASSPKLAHLNAVYDALV 485
DB 493 LATSPPEPMNLQEEFVTLKSLILNSVYTFLSSTKSLPEKHILHVLDTITLH 552
QY 386 VIAKSGISSQOOSMRLANLMLLSHVHASNKGHEHLNMKKKNVYVYDILLMLNAH 445
DB 553 LMAKATLIGQGHPLAQIILISHIHMSNKGHEHLNMYCKKNVYVYDILLMLNAH 612
QY 446 VL 447
DB 613 VL 614

RESULT 24
US-09-903-876-1
Sequence 1; Application US/0990876
Patent No. US20020072587A1
GENERAL INFORMATION:
APPLICANT: Xu, Zhao-Bao
APPLICANT: Somers, William

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Gruyery Match	30-18;	Scores	760;	DB	102;	Length	660;	
Fast Local Similarity	58-79;	Pred. No.	3, 1e-59;					
Mutations 142;	Conservative	57;	Mismatches	39;	Indels	4;	Gaps	3;

Query Match	29.48%	Score 751	138.10%	Length 6602
Host Local Similarity	58.48%	Prod No. 1	96.54%	
Matches 141	Conservative 57	Mismatches 40	Indels 4	Gaps 3
QY	209	ALSPEDVLTLEAPPHVLSR-VSPAPTEASMMSTFKRLADKELVHMSNAKKVPCP	266	
DB	474	SLTADQVSAIIDAEPP-ILYSEYDPPTPEFSAASMGCLTFMIAURELVHMSNAKKVPCP	442	
QY	267	VELSTEDVRIKLLSCTMMVETMMGLMMRSTHQRKLLFAPRLVLDRODKVEDELEFPM	426	
DB	444	VQPLFHQVCHLLFVAMLEFLMGLVWMSRDEHVAFLFAPRLLDPPQVSKVEMVELEFPM	492	
QY	527	LEATISREPELKQREYLVNAMLQVSNMYPVYIALQVADSSKRLAHINAAVITAV	485	
DB	494	LEATISREPEMMNIGCEPEVCEKSLILNSVYVPLSSLEKQDQBRVGLNIDIL	552	
QY	486	WVIAKSTISQVQSGNGLMLMLSHVHVASNKGMBHLLMMKKNVAVYVLDLLEMAH	445	
DB	554	HLMAKGLITLQOQHRLADLLLSHILRMSNKGMEHLYSKKKNVAVYVLDLLEMAH	612	
QY	446	VL447		
DB	614	RL614		

RESULT 27
 US1044584-1
 sequence 1. Application US/1044584

1 APPLICANT: Xiao, Jia Hao
 2 APPLICANT: Kusari, Jyotirmoy
 3 APPLICANT: Chandraratna, Koshanitha A.
 4 TITLE OF INVENTION: Methods of Screening for Compounds That
 5 TITLE OF INVENTION: Modulate Hormone Receptor Activity
 6 FILE REFERENCE: P-AR 4681
 7 CURRENT APPLICATION NUMBER: US/09/922-226
 8 PRIOR APPLICATION NUMBER: US 60/294,797
 9 PRIOR FILING DATE: 2001-04-18
 10 NUMBER OF SEQ ID NOS: 191
 11 SOFTWARE: FastSeq for Windows Version 4.0
 12 SEQ ID NO 2
 13 LENGTH: 533
 14 TYPE: PRT
 15 ORGANISM: Homo sapiens
 16 US-09-922-226-2

Query Match 18.2% Score 458.5; DH 9; Length 533;
 Best Local Similarity 40.2%; Pred. No. 1,90-32;
 Matches 140; Conservative 63; Mismatches 163; Indels 97; Gaps 17;

1 9 VTNI PGSPGRTSPNVIWPTPGH SPTVVHPSL SHIYAPQSPWCFAPSTFRTIPVN 67
 2 136 ISSMSGSPGIPPPAP-----PG-----FSQVSSPVINSTV---SLPGGG 172
 3 68 -PTTRKPVSSNR--CASVTPGSKEDAHGAVSCVASCYVGVWSTGYATPY 121
 4 173 SPPETVYKPVVIVVWVHPPGPGVZAK--RICAIGDPSGKHVYVYSPGVGVGF 230
 5 122 PGLGCHNYGPPATNLTTHKPKPKSGVAPLPGCVGVWVKGSGPPGPGVPIVHGS 181
 6 241 FTIKRLTYSPGVKSTVCPVPRVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 282
 7 182 AHGIPVCAVAPVSGVAPVPELITVALSTVCA VTTIPAPVPIV 229
 8 283 KKKK-----GPPVZAG-----APPEVPIVPIIAP--LAVGYSQGVVGP 322
 9 210 -SPPAPTESSMMKSTKLAKETLVMISMAKLTGVVSLSTVYVPLTFVW 282
 10 423 GGTGSSSSPMPVPT-----NICQAKKSLFLEVWAKLTGVVSLSTVYVPLTFVW 376
 11 283 MEVIMMGLMWSSTHHPKLTIPADLVLDKPGCVSTTIPIMILA-TTSPEELKDH 341
 12 477 NEITLASHSHSTIVPGLIATGIVHNPNSANSA-GVCAITFVPIVTEI VSKRPMIMM 435
 13 442 KPVGVKAMLLNSMTEVATVGVAVSSKLAHLI NAVTDAVWVIAKSTSSQGSNR 401
 14 436 TELGTPATII FNPVAKG-----SNPSEVVI PRVYVASI FTYCRGKYVPGG--P 485
 15 402 LANILMLISVHVASNGMEHLMKCKNVVPVYDILEMLNA 444
 16 486 FAKLLLPALPSIGLKTEHLEFFKLTGTPIDTLEMLNA 528

RESULT 33
 1 US-10-098-184-2
 2 Sequence 2; Application US/10098184
 3 Publication No. US2003010533A1
 4 GENERAL INFORMATION:
 5 APPLICANT: Plahl, Mannus
 6 APPLICANT: Tachdjian, Catherine
 7 APPLICANT: Al-Shamma, Hussein A
 8 APPLICANT: Fanjul, Andrea
 9 APPLICANT: Pleyner, David P.M.
 10 APPLICANT: Spruce, Lyle W.
 11 APPLICANT: Fine, Richard
 12 APPLICANT: Zapf, James W.
 13 TITLE OF INVENTION: RXR ACTIVATING M-LECULES
 14 FILE REFERENCE: 14099, 001602
 15 CURRENT APPLICATION NUMBER: US/10/098,184
 16 CURRENT FILING DATE: 2002-03-08
 17 PRIOR APPLICATION NUMBER: 60/274,342

1 PRIOR FILING DATE: 2001-03-08
 2 NUMBER OF SEQ ID NOS: 3
 3 SOFTWARE: FastSeq for Windows Version 4.0
 4 SEQ ID NO 2
 5 LENGTH: 533
 6 TYPE: PRT
 7 ORGANISM: Artificial Sequence
 8 FEATURE INFORMATION: Description of Artificial Sequence: No. US2004010533A1
 9 OTHER INFORMATION: synthetic construct
 10 US-10-098-184-2

Query Match 18.2% Score 458.5; DH 9; Length 533;
 Best Local Similarity 40.2%; Pred. No. 1,90-32;
 Matches 140; Conservative 63; Mismatches 163; Indels 97; Gaps 17;

1 9 VTNI PGSPGRTSPNVIWPTPGH SPTVVHPSL SHIYAPQSPWCFAPSTFRTIPVN 67
 2 136 ISSMSGSPGIPPPAP-----PG-----FSQVSSPVINSTV---SLPGGG 172
 3 68 -PTTRKPVSSNR--CASVTPGSKEDAHGAVSCVASCYVGVWSTGYATPY 121
 4 173 SPPETVYKPVVIVVWVHPPGPGVZAK--RICAIGDPSGKHVYVYSPGVGVGF 230
 5 122 PGLGCHNYGPPATNLTTHKPKPKSGVAPLPGCVGVWVKGSGPPGPGVPIVHGS 181
 6 241 FTIKRLTYSPGVKSTVCPVPRVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 282
 7 182 AHGIPVCAVAPVSGVAPVPELITVALSTVCA VTTIPAPVPIV 229
 8 283 KKKK-----GPPVZAG-----APPEVPIVPIIAP--LAVGYSQGVVGP 322
 9 210 -SPPAPTESSMMKSTKLAKETLVMISMAKLTGVVSLSTVYVPLTFVW 282
 10 423 GGTGSSSSPMPVPT-----NICQAKKSLFLEVWAKLTGVVSLSTVYVPLTFVW 376
 11 283 MEVIMMGLMWSSTHHPKLTIPADLVLDKPGCVSTTIPIMILA-TTSPEELKDH 341
 12 477 NEITLASHSHSTIVPGLIATGIVHNPNSANSA-GVCAITFVPIVTEI VSKRPMIMM 435
 13 442 KPVGVKAMLLNSMTEVATVGVAVSSKLAHLI NAVTDAVWVIAKSTSSQGSNR 401
 14 436 TELGTPATII FNPVAKG-----SNPSEVVI PRVYVASI FTYCRGKYVPGG--P 485
 15 402 LANILMLISVHVASNGMEHLMKCKNVVPVYDILEMLNA 444
 16 486 FAKLLLPALPSIGLKTEHLEFFKLTGTPIDTLEMLNA 528

RESULT 34
 1 US-09-922-226-3
 2 Sequence 3; Application US/09922226
 3 Publication No. US2003007766A1
 4 GENERAL INFORMATION:
 5 APPLICANT: Zhao, Yi
 6 APPLICANT: Hachey, Scott M.
 7 APPLICANT: Xiao, Jia Hao
 8 APPLICANT: Kusari, Jyotirmoy
 9 APPLICANT: Chandraratna, Koshanitha A.
 10 TITLE OF INVENTION: Methods of Screening for Compounds That
 11 TITLE OF INVENTION: Modulate Hormone Receptor Activity
 12 FILE REFERENCE: P-AR 4681
 13 CURRENT APPLICATION NUMBER: US/09/922-226
 14 CURRENT FILING DATE: 2002-01-09
 15 PRIOR APPLICATION NUMBER: US 60/284,797
 16 PRIOR FILING DATE: 2001-04-18
 17 NUMBER OF SEQ ID NOS: 191
 18 SOFTWARE: FastSeq for Windows Version 4.0
 19 SEQ ID NO 3
 20 LENGTH: 463
 21 TYPE: PRT
 22 ORGANISM: Homo sapiens
 23 US-09-922-226-3

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Search completed: June 16, 2003, 13:41:51
Job time : 53.9571 secs

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A:Residues: 1-595 <GR2>
 A:Cross-references: GR: X61635; NID:931233; FIRM:CAA3284.1; PIR: Q31234
 K:Enzymes:K01001, M. Green, S. Chandon, P.
 EMBL J. 7, 3385-3388, 1988
 A:Title: Genomic organization of the human estrogen receptor gene.
 A:Reference number: A43021; MIM: 8004079; PMID: 314193
 A:Accession: A43021
 A:Molecule type: DNA
 A:Residues: 143-161, 205-225, 244-264, 356-374, 377-376, 402-422, 447-460, 477-492, 508-528
 R:Keywords: M. Kiser, J. G. Gannon, P.
 DNA Seq. 2, 447-458, 1992
 A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
 A:Reference number: S27140; MIM: 93075998; PMID: 1476547
 A:Accession: S27143
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-115 <KEA>
 A:Cross-references: EMBL: X62472; NID: 931231; FIRM: CAA4192.1; PIR: Q31234
 K:Protein, U. J. Pecarotta, E. J. Castagnetta, L. J. Vidali, G.
 Cancer Res. 54, 741-743, 1993
 A:Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive
 A:Reference number: S14000; MIM: 93153765; PMID: 791651
 A:Accession: S14000
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 216-254, 367-399, 437-401, 433-434, 435-436
 A:Cross-references: EMBL: X73067; NID: 9579865; FIRM: CAA51528.1; PIR: Q33986
 A:Note: The authors translated the codon GCG for residue 400 as Val
 R:Protein, H. J. Alkhalaf, M. J. Murphy, L. C.
 Mol. Endocrinol. 6, 773-785, 1992
 A:Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.
 A:Reference number: A41925; MIM: 92293154; PMID: 1604086
 A:Accession: A41925
 A:Molecule type: mRNA
 A:Residues: 1-214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 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611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 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1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 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2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 222

Best local similarity: 49.59, Pval: 5.6e-07
 Matches: 266, Conservative: 74, Mismatches: 121, Indels: 70, Gaps: 14

QY 4 YSLP-----SNVTNFRPRPQQTSPNVTWPTPCHSPVWHPQSHIYAPRQKSP 53
 DB 88 YSLPFLTPNGPSPGSLGSLGSP---ISPLVGVSSPRLSPFM--HPSHHYLETSTP 141
 QY 54 WCFARSLHPTLVNRETLKRYKSNR---CASPVTPGS-----KRIAHGAVCSYA 103
 DB 142 WYSS-----HQAASRHDPGSGSRPQSTGELACAGAGGPEMAKIDRECAVCSYA 194
 QY 104 SGHAYGVMSDEGKAFKRSITGHNHYTPATNPTTIKRPKSGVAPFLPRVYVAVK 163
 DB 194 SGHAYGVMSDEGKAFKRSITGHNHYTPATNPTTIKRPKSGVAPFLPRVYVAVK 253
 QY 164 GSPRPVGVPLVWPGP-----SADPQLHACAKKPS--GCHAPRVRELL 207
 DB 254 GSPRPVGVPLVWPGP-----SADPQLHACAKKPS--GCHAPRVRELL 311
 QY 208 DALSPQVLTILFAEPPIVLLSR--SAPTEASMMMSLTKLAKELVHMSAKKRLPG 265
 DB 412 TSLPPLVLLLGAGPP--ILCSROKLSRPYLEVIMMILTISMAKELVHMSAKKRLPG 370
 QY 266 FVELSLFDQVRLLESFWMEMVMKIMWSTFPRKLLFAPLVLPDEKVEGSLLEFD 325
 DB 371 FVELSLFDQVRLLESFWMEMVMKIMWSTFPRKLLFAPLVLPDEKVEGSLLEFD 430
 QY 326 MLATTSRPEELKQREYLVKAMLLNSSWYPIVATQD--ALSSPKLAHLNAVITAL 384
 DB 431 MLATTSRPEELKQREYLVKAMLLNSSWYPIVATQD--ALSSPKLAHLNAVITAL 490
 QY 385 VWVYAKSGISSQOQSRNLMLLSHVHASKNGEHLINMKCNVVPVYDLLEMLNA 444
 DB 491 IHTLSQGTIACQDARQALLLLSHIFHMSNKGSHLYSMCKCNVVPVYDLLEMLNA 550
 QY 445 HVL-----PVRKS-----STGSPSPAPVSPVSPSSQNP 474
 DB 551 HRLHHVRAQSLSDVDRDPSPSSQSGGLAPGSISASGRLESP 595

RESULT 11

80K estrogen receptor - human
 CSpecies: Homo sapiens (man)
 CDate: 28-Oct-1996 #sequence_revision 13 Mar-1997 #local_change 20 Aug-1999
 CAccession: S64737
 Krogans, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Whitlam, T.
 Nucleic Acids Res. 24, 962-969, 1996
 ATitle: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and
 AReference number: S64737, MIMD:96174665, PMID:R600466
 AAccession: S64737
 AStatus: preliminary; nucleic acid sequence not shown; translation not shown
 A molecule type: mRNA
 AResidues: 1701 <PDB>
 ACross-references: EMBL:047678; NID:q1197854; PDB:AA00115.1; PID:q1197855
 ANote: The nucleotide sequence was submitted to the EMBL data library, January 1996
 CKeywords: estrogen receptor; erba transforming protein homology
 CKeywords: steroid hormone receptor; zinc finger
 E131-456/Domain: erba transforming protein homology <EMBL>
 E131-456/Domain: erba transforming protein homology #aligns of protein: 887

Query Match: 45.48; Score 114.5; DB 2; Length 701
 Best local similarity: 42.48; Pval: 3.7e-83
 Matches: 266, Conservative: 83, Mismatches: 99, Indels: 14, Gaps: 14

QY 10 TNEGPGPG-----TSPVNLMPPTGHLSP-LVHROLSHYATPG 50
 DB 76 TGLPYGSGFAAAGFSGNSGAGFPPIVNSVSPSPMLTHPPGSPFGPQPGVVPYVTFP 135
 QY 51 KSIWCT--EARSLEHTLVNRETLKRYKSNR--CASPVTPGSP-----SKPAAHCAVCSYA 103
 DB 136 PSNVTYVFAVSPAPVTPP-----NSINPFGGSHPEPASTINRQSSMAHCAV119V7AV-NIYA 192

QY 193 SGHAYGVMSDEGKAFKRSITGHNHYTPATNPTTIKRPKSGVAPFLPRVYVAVK 252
 DB 194 SGHAYGVMSDEGKAFKRSITGHNHYTPATNPTTIKRPKSGVAPFLPRVYVAVK 311
 QY 164 GSPRPVGVPLVWPGP-----SADPQLHACAKKPS--GCHAPRVRELL 207
 DB 254 GSPRPVGVPLVWPGP-----SADPQLHACAKKPS--GCHAPRVRELL 311
 QY 208 DALSPQVLTILFAEPPIVLLSR--SAPTEASMMMSLTKLAKELVHMSAKKRLPG 265
 DB 412 TSLPPLVLLLGAGPP--ILCSROKLSRPYLEVIMMILTISMAKELVHMSAKKRLPG 370
 QY 266 FVELSLFDQVRLLESFWMEMVMKIMWSTFPRKLLFAPLVLPDEKVEGSLLEFD 325
 DB 371 FVELSLFDQVRLLESFWMEMVMKIMWSTFPRKLLFAPLVLPDEKVEGSLLEFD 430
 QY 326 MLATTSRPEELKQREYLVKAMLLNSSWYPIVATQD--ALSSPKLAHLNAVITAL 384
 DB 431 MLATTSRPEELKQREYLVKAMLLNSSWYPIVATQD--ALSSPKLAHLNAVITAL 490
 QY 385 VWVYAKSGISSQOQSRNLMLLSHVHASKNGEHLINMKCNVVPVYDLLEMLNA 444
 DB 491 IHTLSQGTIACQDARQALLLLSHIFHMSNKGSHLYSMCKCNVVPVYDLLEMLNA 550
 QY 445 HVL-----PVRKS-----STGSPSPAPVSPVSPSSQNP 474
 DB 551 HRLHHVRAQSLSDVDRDPSPSSQSGGLAPGSISASGRLESP 595

RESULT 12

80K estrogen receptor - Atlantic salmon (fragment)
 CSpecies: Salmo salar (Atlantic salmon)
 CDate: 13-Jan-1996 #sequence_revision 01-Mar-1996 #local_change 20 Aug-1999
 CAccession: S58224
 Krogans, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Whitlam, T.
 Submitted to the EMBL data library, July 1995
 AReference number: S58224
 AAccession: S58224
 AStatus: preliminary
 A molecule type: mRNA
 AResidues: 1535 <EMBL>
 ACross-references: EMBL:X69953; NID:q92901; PDB:CAAG139.1; PID:q92902
 CKeywords: estrogen receptor; erba transforming protein homology
 CKeywords: steroid hormone receptor; zinc finger
 E103-482/Domain: erba transforming protein homology <EMBL>

Query Match: 45.08; Score 114.5; DB 2; Length 535
 Best local similarity: 48.88; Pval: 1.8e-82
 Matches: 246, Conservative: 73, Mismatches: 114, Indels: 71, Gaps: 15

QY 17 GROTSPNVLMPTGHLSP-LVHROLSH-----LYAEQKSPWCFARSLHPTLVNRET 70
 DB 17 GROTSPNVLMPTGHLSP-LVHROLSH-----LYAEQKSPWCFARSLHPTLVNRET 134
 QY 73 PTFVYVNSFASLV--NSGF--FVAHIVAVSTAVSYBYVWSTVSPVATVYVPT 124
 DB 73 PTFVYVNSFASLV--NSGF--FVAHIVAVSTAVSYBYVWSTVSPVATVYVPT 184
 QY 127 GSRHVGSLAASCTIDGSGFSSGAGFPLEVYVAVV--ARBRQCYRVRPQPSMA 184
 DB 127 GSRHVGSLAASCTIDGSGFSSGAGFPLEVYVAVV--ARBRQCYRVRPQPSMA 241
 QY 134 GSHNTPGPAVNTGTPRPNKRSQVCELRKVEVMWAGHLEKPG--GVVYLRK----- 187
 DB 134 GSHNTPGPAVNTGTPRPNKRSQVCELRKVEVMWAGHLEKPG--GVVYLRK----- 241
 QY 185 GHRP AGKAP-----SGR--ATVPEHLLAVPEP 215
 DB 185 GHRP AGKAP-----SGR--ATVPEHLLAVPEP 273
 QY 215 GHRP AGKAP-----SGR--ATVPEHLLAVPEP 273
 DB 215 GHRP AGKAP-----SGR--ATVPEHLLAVPEP 273

Species: Mus musculus (house mouse)
 Date: Jan-1996 #Sequence: revised 01-Mar-1996 #text_change 20 Sep 1996
 Accession: S58087
 R:Pettersson, K.; Svensson, K.; Mattsson, P.; Carlsson, R.; Ohlsson, R.; Bergstrom, A.
 Submitted to the EMBL Data Library, July 1995
 A:Description: Expression of a novel member of estrogen response element-binding protein
 A:Reference number: S58087
 A:Accession: S58087
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-433 <PEP>
 A:Cross-references: EMBL: X89594, NID:4914855, PINN:CAA61756.1, PID:4914856
 C:Keywords: unassigned eta-related proteins; eta transforming protein homology
 C:Keywords: steroid hormone receptor; zinc finger
 F:101-352/Domain; eta transforming protein homology <ERBA>

Query Match 24.58; Score 617; DB 2; Length 433;
 Best local similarity 38.79; Pred. No. 2, 30-41;
 Matches 139; Conservative 76; Mismatches 108; Indels 36; Gaps 10;

QY 96 CAACSYASGYHGVASGECGKAFKRSIQGHNYTCATNCTIDKPKKSCAGRLK 155
 DB 103 CACGACASGYHGVASGECGKAFKRTIQGHNYTCATNCTIDKPKKSCAGRLK 152
 QY 156 CTEVGVWVKQNSP--PFGGCVLPVPSADE---GLHCAKAKKSGCHAPVEPILIA 209
 DB 163 CLKVMIKQVRIIPVPSADEGKVKRHLSTNSPYLNLPSFAKPT-----LTSVSNL 216
 QY 210 LSHQGLVLTLLAPPHVILSRPSADPFEASMMSTIKLAKELVHMSMAKKIDGVEL 269
 DB 217 LSEVQ---DKIYAMPN-----DPEEDIKALTLCEIADPELFLNMKHHIDGPESL 267
 QY 270 STEVAVPIPSGWEVLMKIMKPSIDHPEKILHNDVLDPEKSCPELLEHMLIA 279
 DB 268 TLHDSMTIQSAMPTITGIVKPSIPIYKTLAVEDTIDEEHSPIVCLDIPKALDQ 324
 QY 330 TTSFRELKIQHREYLAKAMILLNS-SMYPELVATDADSSKRLAHLLN-AVPIALVAV 387
 DB 327 LTVPEYKKIKVKEFEFFIKALAIANSTMY-----LENI FAVGKIDGDIHEMGLVEL 379
 QY 384 IAKSSTISSGGSMPANIMIMLSHVPASNKCEHLLNPKCNVAVPTULLEMLNAMY 416
 DB 380 -----SQRDEPRKAKRIWLPILRQIAKAVGHFYSVKIQKVMKRI FLEML EAVV 433

RESULT 16
 A29345
 Steroid hormone receptor ERK1 precursor - human
 N:Alternative names: estrogen-related receptor
 C:Species: Homo sapiens (man)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Sep-1999
 A:Accession: A29345; A19074
 R:Giguere, V.; Vaud, N.; Segall, P.; Evans, P. M.
 Nature 331, 91-94, 1988
 A:Title: Identification of a new class of steroid hormone receptors.
 A:Reference number: A29345; MID:98122545; PMID:3257293
 A:Accession: A29345
 A:Molecule type: mRNA
 A:Residues: 1-521 <GTC>
 A:Cross-references: EMBL: X51416, NID:496608; EIDN:CAA55778.1; PID:4936609; EMBL: Y00290
 K:Miller, S.R.; Kraus, P.T.; Zou, F.; Murray, F.E.; Lott, P.; Murray, T.F.
 Genes Dev. 7, 2297-2319, 1993
 A:Title: SV40 early-late switch involves titration of cellular transcription factors
 A:Reference number: A49074; MID:94040741; PMID:8224847
 A:Accession: A49074
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 166-169, X, 171-173 <WIL>
 C:Superfamily: unassigned eta-related proteins; eta transforming protein homology
 C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; N
 F:174-434/Domain; eta transforming protein homology <ERBA>
 F:176-196/Region; zinc finger
 F:212-216/Region; zinc finger

Query Match 23.44; Score 594.5; DB 2; Length 521;
 Best local similarity 39.68; Pred. No. 1, 80-92;
 Matches 149; Conservative 54; Mismatches 142; Indels 41; Gaps 9;

QY 86 GGG-----SKRIAMHFAVSYASGYHGVASGECGKAFKRSIQGHNYTCATN 136
 DB 157 GGGGGGGGKLVISIPKRLGVASGYHGVASGECGKAFKRTIQGHNYTCATN 216
 QY 137 CTEVGVWVKQNSP--PFGGCVLPVPSADE---GLHCAKAKKSGCHAPVEPILIA 190
 DB 217 CTEVGVWVKQNSP--PFGGCVLPVPSADE---GLHCAKAKKSGCHAPVEPILIA 276
 QY 191 KARSCHAPREVELLDLSPQVLTLELPHVLI-SRPSAPTEASMMSTIKLA 249
 DB 277 PLAVGVNA---PRTAAVNA-----LVSHLLVPEKIVAMPDAPDCHLPAVATIDOLF 329
 QY 250 FRELVMISMAKKIPGVEISLFDGVRLKESGWEVLMKIMKPSIDHPEKILHNDVLD 309
 DB 330 PREIVVISMANSITPSSLSLSDQMSVLSQWMEVLDVAVAPSLIPDIEAFARDELVL 389
 QY 410 DPEGKAVPSIIFEDIMLATTSPPEIKIQHREYLAKAMILLNS-SMYPELVATDADSS 369
 DB 490 D-EEGAPAAQIGELFAILLVPRDLALRELEEVLLKALAIANSDVHLEDEPRIMSS 448
 QY 470 SEPTAHINAVTDVAV-VWIAKSGISSGGSMPANIMIMLSHVPASNKCEHLLNPKCN 428
 DB 449 CTKTII-----PAILPFRAGDAGGACAPPRAPACRITIDGILRQIAKVAIDHGVK 502
 QY 429 KNPVYEDLLLEMLNA 444
 DB 503 ECKVPMKLEFLEMLFA 518

RESULT 17
 A39596
 Progesterone receptor B form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Apr-1999
 A:Accession: A39596; 149111
 R:Shiota, C.R.; Shymala, G.; Schneider, W.; Parry, G.
 Biochemistry 30, 7014-7020, 1991
 A:Title: Molecular cloning, sequence analysis, and expression of complementary DNA on
 A:Reference number: A39596; MID:91299759; PMID:2069958
 A:Accession: A39596
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-923 <STH>
 A:Cross-references: GB: M68915, GB: J05333, NID:4200471, PINN:AAA39771.1, PID:4200472
 R:Bashir, K.; Wu-Peng, X.S.; Fushashi, T.; Kato, J.; Platt, D.W.
 Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
 A:Title: Nucleic acid sequence and DNAse hypersensitivity sites of the 5' region of the
 A:Reference number: 149111; MID:94100413; PMID:7602647
 A:Accession: 149111
 A:Status: preliminary; translated from GB/EMBL/DDHL
 A:Molecule type: DNA
 A:Residues: 1-9 SHAG
 A:Cross-references: EMBL: U12644; NID:9639916; PINN:AAA66067.1; PID:9639917
 C:Superfamily: progesterone receptor; eta transforming protein homology
 C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;
 F:557-577/Region; eta transforming protein homology <ERBA>
 F:553-617/Region; zinc finger

Query Match 18.58; Score 466.5; DB 2; Length 923;
 Best local similarity 30.98; Pred. No. 5, 80-92;
 Matches 114; Conservative 65; Mismatches 115; Indels 75; Gaps 13;

QY 96 CAACSYASGYHGVASGECGKAFKRSIQGHNYTCATNCTIDKPKKSCAGRLK 155
 DB 557 CACGACASGYHGVASGECGKAFKRTIQGHNYTCATNCTIDKPKKSCAGRLK 616
 QY 156 CTEVGVWVKQNSP--PFGGCVLPVPSADE---GLHCAKAKKSGCHAPVEPILIA 209


```

144 KTLKKLTYSYVYKNGKTVYKNGYVYVYKTLADYMKRFAVYFT
182 ACPQQLRACAKKSGSHAKVRLALSLPQL VTIILAEPRVLL
196 KKKD GGGGAGG-----APEDMVDRIILAE--LAVESKSGVDPG 245
240 -----SRSAFTFASMMSTKLADEKIVIMISWAKIPGVNLSLPQVLLNSGW 282
246 GATGGGSSNDPVT-----NVCAGAKGULFTYVWAKRIPHSLSLLDPVYLLAKGM 289
284 MEVIMGLMMSSTIDHKKLIFADYVLDDEKCVGSLLEFDMLLA-TISPERKLIQH 341
290 NEILLASFHSRSDVMDMLTLATGLHVRNSASHA-GVCAITELVITELYSKMEKEMK 346
442 KEVIAKAMLLNSSWYPIVTAQVDSKRLAHLLNAVTDALVWVAKSSLSQGSMSR 401
449 TELAKTALLPMDAKL-----SNRCVEILIRKVVASILEYVKQKYPFGQG-R 498
402 IANIMLSIVPASNRMHLLNMCKNVVAVYDILLERMA 444
499 FAKLLRLPALRSLGKLEHLEPKLIGITIDPELMMLCA 441

```

RESULT 22

retinoid X receptor beta - mouse
 c1Species: Mus musculus (house mouse)
 c1Date: 31 Dec 1993 #sequence_revision 41-Dec-1994 #exl_change 02-Aug 2002
 c1Accession: J41727
 c1Date: M.J. Kasturi, P.J. Lyons, R.J. Nakhlati, H. Saunders, M.J. Zacharewski, T.J. Chan, Cell 66, 377-395, 1992
 A>Title: Purification, cloning, and RXR identity of the beta cell factor with which RXR
 A1Reference number: A41727, MIM:9212795, PMID:119259
 A1Accession: J41727
 A1Status: nucleic acid sequence not shown
 A1Molecule type: mRNA
 A1Accession: J448-1651
 A1Expected local source: liver
 A1Notes: Sequence extracted from MCF1 boe-bone (MIM:177547)
 c1Genot test:
 A1Start codon: cct
 c1Superfamily: retinoid acid receptor alpha; c1bA transforming protein homology
 c1Keywords: zinc finger
 F118 664/664main: c1bA transforming protein homology - ERBA-

Query Match 18.1% Score 455.5; DB 2; Length 448;
 Best Local Similarity 40.2%; Pred. No. 1,86-28;
 Matches 140; Conservative 62; Mismatches 164; Indels 97; Gaps 17;

```

9 VTNIDGTPGQTTSPVIMPTDLSPIVNHQLSHLVAEYKSWCAKSLHLLPVN 67
144 KTLKKLTYSYVYKNGKTVYKNGYVYVYKTLADYMKRFAVYFT
196 KKKD GGGGAGG-----APEDMVDRIILAE--LAVESKSGVDPG 245
240 -----SRSAFTFASMMSTKLADEKIVIMISWAKIPGVNLSLPQVLLNSGW 282
246 GATGGGSSNDPVT-----NVCAGAKGULFTYVWAKRIPHSLSLLDPVYLLAKGM 289
284 MEVIMGLMMSSTIDHKKLIFADYVLDDEKCVGSLLEFDMLLA-TISPERKLIQH 341
290 NEILLASFHSRSDVMDMLTLATGLHVRNSASHA-GVCAITELVITELYSKMEKEMK 346
442 KEVIAKAMLLNSSWYPIVTAQVDSKRLAHLLNAVTDALVWVAKSSLSQGSMSR 401
449 TELAKTALLPMDAKL-----SNRCVEILIRKVVASILEYVKQKYPFGQG-R 498
402 IANIMLSIVPASNRMHLLNMCKNVVAVYDILLERMA 444
499 FAKLLRLPALRSLGKLEHLEPKLIGITIDPELMMLCA 441

```

```

442 KEVIAKAMLLNSSWYPIVTAQVDSKRLAHLLNAVTDALVWVAKSSLSQGSMSR 401
449 TELAKTALLPMDAKL-----SNRCVEILIRKVVASILEYVKQKYPFGQG-R 498
402 IANIMLSIVPASNRMHLLNMCKNVVAVYDILLERMA 444
499 FAKLLRLPALRSLGKLEHLEPKLIGITIDPELMMLCA 441

```

RESULT 24

retinoid acid receptor coregulator - rat
 c1Species: Rattus norvegicus (Norway rat)
 c1Date: 28 May 1992 #sequence_revision 29-May-1998 #exl_change 02-Aug 1999
 c1Accession: A41651
 c1Date: V.C. DeSoto, C. Andersen, B.J. Hollaway, J.M. Devery, O.V. Naveet, A.M. Ki
 Cell 67, 1251-1266, 1991
 A>Title: RXRbeta: a coregulator that enhances binding of retinoid acid, thyroid hormo
 A1Reference number: A41651, MIM:92104690, PMID:1662118
 A1Accession: A41651
 A1Status: preliminary
 A1Molecule type: mRNA
 A1Accession: J451-70A
 A1References: GR:M8176; NID:9206602; PID:AAA2055.1; PID:9206601
 c1Superfamily: retinoid acid receptor alpha; c1bA transforming protein homology
 c1Keywords: zinc finger
 F121 397/397main: c1bA transforming protein homology - ERBA-

Query Match 18.1% Score 455.5; DB 2; Length 451;
 Best Local Similarity 40.2%; Pred. No. 1,86-28;
 Matches 140; Conservative 62; Mismatches 164; Indels 97; Gaps 17;

```

9 VTNIDGTPGQTTSPVIMPTDLSPIVNHQLSHLVAEYKSWCAKSLHLLPVN 67
144 KTLKKLTYSYVYKNGKTVYKNGYVYVYKTLADYMKRFAVYFT
196 KKKD GGGGAGG-----APEDMVDRIILAE--LAVESKSGVDPG 245
240 -----SRSAFTFASMMSTKLADEKIVIMISWAKIPGVNLSLPQVLLNSGW 282
246 GATGGGSSNDPVT-----NVCAGAKGULFTYVWAKRIPHSLSLLDPVYLLAKGM 289
284 MEVIMGLMMSSTIDHKKLIFADYVLDDEKCVGSLLEFDMLLA-TISPERKLIQH 341
290 NEILLASFHSRSDVMDMLTLATGLHVRNSASHA-GVCAITELVITELYSKMEKEMK 346
442 KEVIAKAMLLNSSWYPIVTAQVDSKRLAHLLNAVTDALVWVAKSSLSQGSMSR 401
449 TELAKTALLPMDAKL-----SNRCVEILIRKVVASILEYVKQKYPFGQG-R 498
402 IANIMLSIVPASNRMHLLNMCKNVVAVYDILLERMA 444
499 FAKLLRLPALRSLGKLEHLEPKLIGITIDPELMMLCA 441

```

RESULT 24

retinoid X receptor beta - mouse
 c1Species: Mus musculus (house mouse)
 c1Date: 29 May 1998 #sequence_revision 29-May-1998 #exl_change 02-Aug 1999
 c1Accession: J41727
 c1Date: M.J. Kasturi, P.J. Lyons, R.J. Nakhlati, H. Saunders, M.J. Zacharewski, T.J. Chan, Cell 66, 377-395, 1992

QY 424 FIMLALATSKREKILQHHFVAVAMHIDR SVAIVADGACVSPFLAMAAVAVI 407
 DB 768 CTIMWIDPQFVAVLVSAPFPLQMFVILINLPIELRISQIOLKESKYLIELLA 456
 QY 482 DALVWVIAKSLSSQGSRLANLL 406
 DB 856 ---IGLRKGVSSSSPFGYGLIKL 877

RESULT 29
 S26670

retinotic acid receptor X gamma - mouse
 CSpecies: Mus musculus (house mouse)

CDate: 14-Jan-1995 #sequence_revision 13-Jan-1995 #ext_change 20-Aug-1995

CAccession: S26670

R-Modelshot: 1:1: Portmeyer, H: Hoymer, P A: Zhou, Y: Yang, P S: Cheng, A P: Pohl
 Genes Dev. 6, 329-344, 1992

A>Title: Characterization of three RXR genes that mediate the action of 9-cis retinoic
 AReference number: S26668; M010-92192447; PMID:1312497

AAccession: S26670

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1 463 768

A:Cross references: EMBL X6225, NID 35405, PDB 5AA564, FID 42492

C:Superfamily: retinoic acid receptor alpha; erba transforming protein homology

C:Keywords: zinc finger

F117-379/40main: erba transforming protein homology - ERBA

Query Match 17.6% Score 443 DB 2: Length 463
 Best Local Similarity 27.8% Pred. No. 1.8e-27
 Matches 135; Conservative 69; Mismatches 205; Indels 76; Gaps 13.

QY 2 NYS-----ISNNTNLEGGRGROTTSPNVLMPT-----PGHL-SPLVHQLSLVAEP 49
 DB 4 NYSHEKRPFGSGSGHSTGSMSPVALPTGKMDSHSTDTDPVAPRLISAV-GTP 62
 QY 50 QKSPWCEAVSEIPTI-----PYNPPTIKKVSNGCAFPV----- 84
 DB 63 LNAIGSPVYVITISAMRPSSGALAAPGILNLVAPSSQLNVNVSASSSLIKRLPRLKIC 122
 QY 85 -----TGDSKRDHRCVAGSDYAGYGVWSGCKKAPFKRSIQGHNDYIGPATNQC 138
 DB 123 NMNVESTSDS LVKHCATGCPSSGKHVYVSSECKGPEKPIIRKILLYTCRQNG 181
 QY 139 TIRKNPKSQAACRIKRYGVNVRKGSRRGGRVLRPQSAIDQIHCAKAKRSQH 198
 DB 182 LIRKQPNQGYVYKCI VMNKRPAVAFEP-----QSPFPAVSFAFCA-----SSSH 231
 QY 199 APRVPELITLALSPEDVLILLEAPPHVILSPSAPFEASMMSTIKLADKELMIS 258
 DB 232 EIDPVERILFA-----ELAVHRTSYGIMVENSTNDQVNIINAAIKOLFTIVE 282
 QY 259 WAKRIQVAVSLTFQVRLIFSWMFVEMKIMMSINHPGELIAPRLVLDPEQKVE 318
 DB 283 WAKRIQVAVSLTFQVRLIFSWMFVEMKIMMSINHPGELIAPRLVLDPEQKVE 318
 QY 319 GILEIFDLIA-LTSPRELKLOHKEVGVKAMILLNSMYPLVATQIAOSKRLAHL 377
 DB 442 GVSSTFQVAVTFVSMKMDQMKSTGCLPAIVLENIPAKGLSNPSEVTLREKVATL 401
 QY 478 NAVTALVWVIAKSLSSQGSRLANLLMLSHVHASNKQREHLNKKYKNVAVYV 437
 DB 402 FAVTKU-----KYPQPKFAKLILRLPAIRSLQKLEHFEKLLGTPIDSF 451
 QY 438 LLEML 442
 DB 452 LLEML 456

RESULT 30
 B41727
 retinoid-X receptor-gamma - mouse

CSpecies: Mus musculus (house mouse)

CDate: 24-Feb-1993 #sequence_revision 31-Dec-1997 #ext_change 02-Apr-2002

CAccession: B41727; A40702; B40702

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: B41727

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Nakshatri, H. Saunders, M. Zdzienicka, T. Chao

Cell 66, 377-395, 1992

A>Title: Purification, cloning, and RXR identity of the R α cell factor with which R

AReference number: A41227; M010-92122555; PMID:1310259

AAccession: A40702

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1 463 461

A:Cross references: GB B84819, NID 4209881, PDB 5AA564, FID 426982

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A:Experimental source: liver

A:Molecule sequence extracted from NCB1 backbone (NCB1:77550)

RefSeq: M. Kastner, P. Lyons, R. Naksh

db 452 LMEML 456

RESULT 41

glucocorticoid receptor African clawed frog

Species: *Xenopus laevis* (African clawed frog)

cdDate: 14 Jun 1995 #sequence revision 27 Oct 1995 #text_change 22 Jun 1999

Accession: S45448; S44047; S42084

RefSeq: X. laevis, E. Peterson Maduro, J. van der Burg, B. Bestier, D.H.J. Blokhuis, Biophys. Acta 1218, 194-198, 1994

Abstract: Expression of the glucocorticoid receptor gene is regulated during early embryo

Accession number: S45448; MIMD:94289478; PMID:8018720

Accession: S45448

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Accession: S45448

db 707 SSCNMGPGYUJFKLLSMEVAVNLAPETLSLTKSSSTDEPRLMSHUSNGLRY 764

RESULT 42

glucocorticoid receptor Japanese eel

Species: *Anguilla japonica* (Japanese eel)

cdDate: 24 Jul 1999 #sequence revision 23 Jul 1999 #text_change 11 May 2000

Accession: J60194

RefSeq: T. Ikenishi, T. Kobayashi, T. Nishikawa, Y. Hirokawa, Biophys. Res. Commun. 254, 478-483, 1999

Abstract: Expression of the glucocorticoid receptor gene is regulated during early embryo

Accession number: J60194; MIMD:99119419; PMID:9918846

Accession: J60194

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Keywords: zinc finger
E:548-806/Jamain, c-ERL transforming protein homology <ERBA>
F:550-570/Region: zinc finger
E:586-610/Region: zinc finger

Query Match	Score	DB 2	Length
17.28	434	911	
10.69	20	25	

Best Local Similarity: 28.6%; Prod. No. 2, 2c-2c;
Matches: 109; Conservative: 72; Mismatches: 108, Indels: 92; Gaps: 14.

[illegible]

Search completed: June 16, 2003, 14:16:36
Job time : 28.4814 secs

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Genforce version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

M protein protein search, using SW model

Run on: June 16, 2003, 07:39:07 ; Search time 12.0675 seconds
(without alignment)

1639 467 Million cell updates/sec

File: US-08-826-361a-5

Perfect score: 2522

Sequence: 1 MARYSHEWTFN PEPDPEST

Scoring table: MIOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 112892 seqs, 4176329 residues

Total number of hits satisfying chosen parameters: 112892

Minimum db seq length: 0

Maximum db seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length DB	ID	Description
1	2522	100.0	540	ESR2_HUMAN	G92731 home sapien
2	2456	99.4	540	ESR2_HUMAN	G92731 home sapien
3	2260	99.2	540	ESR2_MOUSE	G92731 home sapien
4	2249	99.2	540	ESR2_FAT	G92731 home sapien
5	2232.5	98.5	527	ESR2_BOVIN	G92731 home sapien
6	2234.5	98.2	527	ESR2_SHEEP	G92731 home sapien
7	2180	86.4	526	ESR2_PIG	G92731 home sapien
8	1946	76.8	554	ESR2_STUAT	G92731 home sapien
9	1944	76.7	474	ESR2_CHICK	G92731 home sapien
10	1924.5	76.2	474	ESR2_CHICK	G92731 home sapien
11	1453	57.6	573	ESR2_ANGIA	G92731 home sapien
12	1498	55.4	279	ESR2_MOUSE	G92731 home sapien
13	1486	55.0	568	ESR2_MOUSE	G92731 home sapien
14	1471	54.4	568	ESR2_MOUSE	G92731 home sapien
15	1464.5	53.7	673	ESR2_MOUSE	G92731 home sapien
16	1442.5	53.2	576	ESR2_FAT	G92731 home sapien
17	1428	52.4	610	ESR2_MOUSE	G92731 home sapien
18	1422.5	52.4	569	ESR2_MOUSE	G92731 home sapien
19	1408.5	51.9	565	ESR2_MOUSE	G92731 home sapien
20	1401	51.6	567	ESR2_MOUSE	G92731 home sapien
21	1222	48.5	587	ESR1_MOUSE	G92731 home sapien
22	1221	48.4	589	ESR1_CHICK	G92731 home sapien
23	1207	47.9	585	ESR1_SHEEP	G92731 home sapien
24	1204	47.7	595	ESR1_HUMAN	G92731 home sapien
25	1202	47.7	595	ESR1_MOUSE	G92731 home sapien
26	1199.5	47.6	586	ESR1_XENLA	G92731 home sapien
27	1198	47.5	599	ESR1_MOUSE	G92731 home sapien
28	1196	47.4	599	ESR1_MOUSE	G92731 home sapien
29	1194.5	47.4	600	ESR1_FAT	G92731 home sapien
30	1193	47.3	595	ESR1_PIG	G92731 home sapien
31	1192	47.3	620	ESR1_ORYZLA	G92731 home sapien
32	1189.5	47.2	594	ESR1_MOUSE	G92731 home sapien
33	1185.5	47.0	581	ESR1_MOUSE	G92731 home sapien
34	1181	46.8	584	ESR1_MOUSE	G92731 home sapien
35	1177	46.7	585	ESR1_MOUSE	G92731 home sapien
36	1176.5	46.6	599	ESR1_MOUSE	G92731 home sapien
37	1151	45.6	617	ESR1_MOUSE	G92731 home sapien
38	1144	45.4	622	ESR1_MOUSE	G92731 home sapien
39	1141.5	45.0	535	ESR1_MOUSE	G92731 home sapien
40	877	34.8	407	ESR1_MOUSE	G92731 home sapien
41	799.5	31.7	449	ESR1_MOUSE	G92731 home sapien
42	644.5	25.6	438	ESR1_MOUSE	G92731 home sapien
43	630	25.0	438	ESR1_MOUSE	G92731 home sapien
44	630	25.0	500	ESR1_MOUSE	G92731 home sapien
45	617	24.5	433	ESR1_MOUSE	G92731 home sapien
46	593.5	23.5	519	ESR1_MOUSE	G92731 home sapien
47	584.5	23.2	472	ESR1_MOUSE	G92731 home sapien
48	583.5	21.9	174	ESR1_MOUSE	G92731 home sapien
49	456.5	18.5	923	ESR1_MOUSE	G92731 home sapien
50	465	18.4	923	ESR1_MOUSE	G92731 home sapien
51	458.5	18.2	533	ESR1_MOUSE	G92731 home sapien
52	456.5	18.1	377	ESR1_MOUSE	G92731 home sapien
53	455.5	18.1	458	ESR1_MOUSE	G92731 home sapien
54	455.5	18.1	520	ESR1_MOUSE	G92731 home sapien
55	453	18.0	930	ESR1_MOUSE	G92731 home sapien
56	449.5	17.8	758	ESR1_MOUSE	G92731 home sapien
57	449	17.8	457	ESR1_MOUSE	G92731 home sapien
58	448	17.8	933	ESR1_MOUSE	G92731 home sapien
59	443	17.6	463	ESR1_MOUSE	G92731 home sapien
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61	441.5	17.5	776	ESR1_MOUSE	G92731 home sapien
62	440	17.4	463	ESR1_MOUSE	G92731 home sapien
63	439.5	17.4	776	ESR1_MOUSE	G92731 home sapien
64	439	17.4	467	ESR1_MOUSE	G92731 home sapien
65	438.5	17.4	895	ESR1_MOUSE	G92731 home sapien
66	438.5	17.4	895	ESR1_MOUSE	G92731 home sapien
67	438.5	17.4	911	ESR1_MOUSE	G92731 home sapien
68	437.5	17.3	709	ESR1_MOUSE	G92731 home sapien
69	435.5	17.3	777	ESR1_MOUSE	G92731 home sapien
70	435	17.2	777	ESR1_MOUSE	G92731 home sapien
71	435	17.2	777	ESR1_MOUSE	G92731 home sapien
72	435	17.2	777	ESR1_MOUSE	G92731 home sapien
73	434.5	17.2	462	ESR1_MOUSE	G92731 home sapien
74	434.5	17.2	964	ESR1_MOUSE	G92731 home sapien
75	434	17.2	467	ESR1_MOUSE	G92731 home sapien
76	434	17.2	777	ESR1_MOUSE	G92731 home sapien
77	433.5	17.2	884	ESR1_MOUSE	G92731 home sapien
78	433	17.2	981	ESR1_MOUSE	G92731 home sapien
79	432.5	17.2	472	ESR1_MOUSE	G92731 home sapien
80	431.5	17.1	778	ESR1_MOUSE	G92731 home sapien
81	430	17.0	786	ESR1_MOUSE	G92731 home sapien
82	429	17.0	441	ESR1_MOUSE	G92731 home sapien
83	429	17.0	441	ESR1_MOUSE	G92731 home sapien
84	429.5	17.0	509	ESR1_MOUSE	G92731 home sapien
85	428.5	17.0	902	ESR1_MOUSE	G92731 home sapien
86	428	17.0	470	ESR1_MOUSE	G92731 home sapien
87	427.5	17.0	807	ESR1_MOUSE	G92731 home sapien
88	426.5	16.9	899	ESR1_MOUSE	G92731 home sapien
89	426.5	16.9	467	ESR1_MOUSE	G92731 home sapien
90	425.5	16.9	507	ESR1_MOUSE	G92731 home sapien
91	425.5	16.9	907	ESR1_MOUSE	G92731 home sapien
92	424.5	16.8	773	ESR1_MOUSE	G92731 home sapien
93	423	16.7	406	ESR1_MOUSE	G92731 home sapien
94	421	16.7	603	ESR1_MOUSE	G92731 home sapien
95	419.5	16.6	598	ESR1_MOUSE	G92731 home sapien
96	419.5	16.6	784	ESR1_MOUSE	G92731 home sapien
97	415.5	16.5	795	ESR1_MOUSE	G92731 home sapien
98	411	16.3	612	ESR1_MOUSE	G92731 home sapien
99	410	16.3	385	ESR1_MOUSE	G92731 home sapien
100	409	16.3	977	ESR1_MOUSE	G92731 home sapien
101	409	16.2	785	ESR1_MOUSE	G92731 home sapien
102	408.5	16.2	673	ESR1_MOUSE	G92731 home sapien
103	407	16.1	386	ESR1_MOUSE	G92731 home sapien
104	403.5	16.0	508	ESR1_MOUSE	G92731 home sapien
105	397.5	15.8	495	ESR1_MOUSE	G92731 home sapien
106	391.5	15.5	386	ESR1_MOUSE	G92731 home sapien
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107	484.5	15.4	5.98	NR42_HUMAN	P43354	homo sapiens
108	484.5	15.4	5.98	NR42_KAT	G07917	rattus norv
109	484.5	15.4	5.98	NR42_MOUSE	U07219	mus musculus
110	484	15.2	4.80	NR61_HUMAN	P15456	homo sapiens
111	484	15.2	5.60	NR52_MOUSE	P45446	mus musculus
112	483	15.2	4.96	NR21_ORYCTA	G77413	oryzias lat
113	483	15.2	5.41	NR52_HUMAN	G09342	homo sapiens
114	482	15.1	4.47	NR4_F03801	G95583	torus f03801
115	482	15.1	5.01	NR52_CHICK	U04210	gallus gall
116	479.5	15.0	4.58	NR4_XENLA	PE1125	xenopus lae
117	477	14.9	6.28	NR4_FAT	PE1179	rattus norv
118	476	14.9	4.62	NR4_MOUSE	P11416	mus musculus
119	474.5	14.8	4.08	NR4_MOUSE	G94046	mus musculus
120	473.5	14.8	4.47	NR62_MOUSE	P20767	mus musculus

ALLEGMENTS

	RESULT 1
ESR2_HUMAN	STANDARD; PRT= 530 AA.
ID	ESR2_HUMAN
AC	G97271; U60685; G60608; C75584; G60702; G60703; C75583; Q9UGK9;
AF	Q9UGK9; Q9UHD3;
DI	15 JUL 1999 (Ref. 48, Created)
DT	15 JUL 1999 (Ref. 48, last sequence update)
FE	16 OCT 2001 (Ref. 40, last annotation update)
DE	Estrogen receptor beta (ER-beta).
GN	ESR2 OR NR1A2 OR ESRB.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CA	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX	NCBI TaxId 9606;
RN	[1]
RZ	SEQUENCE FROM N.A. (ISOPROB BETA 1).
RX	MEDLINE 98159878; PubMed 9473491;
RA	Ogawa S., Inoue S., Watanabe T., Hiroi H., Orimo A., Hosoi T.,
RB	Onishi Y., Muramatsu M.;
RC	"The complete primary structure of human estrogen receptor beta
RI	(Erbeta) and its heterodimerization with ER alpha in vivo and in
RD	vitro.";
RL	Biochem. Biophys. Res. Commun. 241(1-2):126(1998).
RM	[2]
RZ	SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RP	TESSIE TESTS, and Breast;
RQ	MEDLINE 98400280; PubMed 964657;
RA	Moore L.T., McKee D.D., Slonitz-Koslov K., Moore L.B., Jones S.A.,
RB	Borzo F.L., Su J., Lee, K., Klapper S.A., Lehman J.M., Willson T.M.;
RC	"Cloning and characterization of human estrogen receptor beta
RI	cDNAs.";
RD	Biochem. Biophys. Res. Commun. 247(2-3):78(1998).
RE	[3]
RZ	SEQUENCE OF 48 530 FROM N.A. (ISOPROB BETA-1), AND CHARACTERIZATION
RF	TESSIE TESTS;
RQ	MEDLINE 96454875; PubMed 8769413;
RA	Mosselman S., Feldman J., Injima R.;
RB	"Er beta-4: Identification and characterization of a novel human
RI	estrogen receptor.";
RD	FEBS Lett. 392:49-53(1996).
RE	[4]
RZ	SEQUENCE FROM N.A. (ISOPROB BETA 2/X), AND CHARACTERIZATION.
RF	TESSIE TESTS;
RX	MEDLINE 98337408; PubMed 9671811;
RA	Ogawa S., Inoue S., Watanabe T., Orimo A., Hosoi T., Onishi Y.,
RB	Muramatsu M.;
RC	"Molecular cloning and characterization of human estrogen receptor
RI	beta c-x: a potential inhibitor of estradiol action in human.";
RD	Nucleic Acids Res. 26:3505-3512(1998).
RE	[5]
RZ	SEQUENCE OF 59 530 FROM N.A. (ISOPROB BETA 5A AND BETA-6).
RF	TESSIE ESTROGENISM;
RG	Brandenburg A.W., Lovovic D., Taylor R.N., Jaffe R.B.;
RH	Submitted (JUN 1998) To The EMBL/GenBank/DDBJ databases.

[6] SEQUENCE FROM N.A. (ISOFORM BETA-2A).
RX TISSUE: ovary;
RX MEDLINE:98348489; PubMed 9645228;
RA In R., Leygue E., Dowlaw H., Murphy L., Murphy P.H.;
RT "Estrogen receptor beta mRNA variants in human and murine tissues.";
RL Mol. Cell. Endocrinol. 138:199-204(1998).
RN [17]
RA SEQUENCE OF 1.69 FROM N.A.
RA In L.C., Dattaya R.;
RT "Cloning and characterization of the estrogen receptor beta gene promoter.";
RL Submitted (Oct 1999) to the EMBL/Genbank/Tran databases.
RN [8]
RX CHARACTERIZATION:
RX MEDLINE:97467483; PubMed 9425413;
RA Pace F., Taylor J., Souchard-Boham S., Combès R.C., Ali S.;
RT "Human estrogen receptor beta binds DNA in a manner similar to and
RT dimerizes with estrogen receptor alpha.";
RL J. Biol. Chem. 272:25832-25838(1997).
CC 1-1 FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF ER
CC ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN DEPENDENT MANNER.
CC ISOFORM BETA-1X LACKS LIGAND BINDING ABILITY AND HAS NOT YET ONLY
CC VERY LOW ERE BINDING ACTIVITY RESULTING IN THE LOSS OF LIGAND-
CC DEPENDENT TRANSCRIPTIONAL ABILITY. DNA BINDING BY ER ALPHA AND
CC BETA IS RAPIDLY LOST AT 37 DEGREES CELSIUS IN THE ABSENCE OF
CC LIGAND WHILE IN THE PRESENCE OF 17 BETA ESTRADIOL AND 4-HYDROXY
CC TAMOXIFEN LOSS IN DNA-BINDING AT ELEVATED TEMPERATURE IS MORE
CC GRADUAL.
CC 1-2 SPINDLE BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER
CC ALPHA. ISOFORM BETA-2/1X PREPREFERENTIALLY FORMS A HETERODIMER WITH
CC ER ALPHA RATHER THAN ER-BETA AND INHIBITS DNA BINDING BY ER ALPHA.
CC 1-3 SKELETAL LOCATION: A Isoforms: BETA-1 (SHOWN HERE), BETA-2/1X,
CC BETA-2A, BETA-3, BETA-4, BETA-5, BETA 5A AND BETA-6; ARE PRODUCED
CC BY ALTERNATIVE SPLICING.
CC 1-4 TISSUE SPECIFICITY: ISOFORM BETA-1 IS EXPRESSED IN TESTIS AND
CC OVARY, AND AT A LOWER LEVEL IN HEART, BRAIN, PLACENTA, LIVER,
CC SKELETAL MUSCLE, SPLEEN, THYMUS, PROSTATE, COLON, BONE MARROW,
CC MAMMARY GLAND AND UTERUS. ALSO FOUND IN UTERINE BONE, BREAST, AND
CC OVARIAN TUMOR CELL LINES, BUT NOT IN COLON AND LIVER TUMORS.
CC ISOFORM BETA-2 IS EXPRESSED IN SPLEEN, THYMUS, TESTIS AND OVARY
CC AND AT A LOWER LEVEL IN SKELETAL MUSCLE, PROSTATE, COLON, SMALL
CC INTESTINE, LEUKOCYTES, BONE MARROW, MAMMARY GLAND AND UTERUS.
CC ISOFORM BETA-3 IS FOUND IN TESTIS. ISOFORM BETA-4 IS EXPRESSED IN
CC TESTIS, AND AT A LOWER LEVEL IN SPLEEN, THYMUS, OVARY, MAMMARY
CC GLAND AND UTERUS. ISOFORM BETA-5 IS EXPRESSED IN TESTIS, PLACENTA,
CC SKELETAL MUSCLE, SPLEEN AND LEUKOCYTES, AND AT A LOWER LEVEL IN
CC HEART, LUNG, LIVER, KIDNEY, PANCREAS, THYMUS, PROSTATE, COLON,
CC SMALL INTESTINE, BONE MARROW, MAMMARY GLAND AND UTERUS. NOT
CC EXPRESSED IN BRAIN.
CC 1-5 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC 1-6 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC NKS SUBFAMILY.
CC
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CC or send an email to license@ebi.ac.uk).

DR	PROSTATE, P500011: NUCLEAR RECEPTOR 1.
KM	Receptor: Transcription regulation; DNA-binding; Nuclear protein;
KM	Zinc-finger; Steroid-binding; Alternative splicing; Glycoprotein;
KM	Phosphorylation.
FT	DOMAIN 1 148
FT	DOMAIN 149 214
FT	ZN_FING 149 169
FT	ZN_FING 185 209
FT	DOMAIN 215 530
FT	MOD_RES 61 61
FT	MOD_RES 87 87
FT	MOD_RES 105 105
FT	MOD_RES 488 488
FT	CARRHYD 61 61
FT	VARSELPT 464 464
FT	VARSELPT 319 364
FT	VARSELPT 355 409
FT	VARSELPT 319 409
FT	MUTAGEN 105 105
FT	MUTAGEN 139 139
FT	CONFLICT 47 47
FT	CONFLICT 142 142
FT	CONFLICT 200 200
FT	CONFLICT 378 378
FT	CONFLICT 412 412
FT	CONFLICT 445 445
FT	CONFLICT 511 511
FT	SEQUENCE 530 AA: 59012 MW: 90673A161550ABE4 CR664:
Query Match	89.28; Score 2250; DR 1; Length 530.
Best Local Similarity	88.78; Pred. No. 5; E=178;
Matches 424; Conservative 22; Mismatches 32; Indels 0; Gaps 0.	
UY	1 MNTSPSTVNTLESGRQGTSPNVIWPTPEISPIVPEPQSHIYAFPEISPTAFAS
DB	54 MNTSVSSSTGNLEFGHVPKPTASPNVIMPTSHISPLATGCSNITYAPPEQSPWFA
UY	61 EHTLPVNETKKKYSNGACAVTQPSKRDHPCAVSDVASYHGVMSDECKAF
DB	114 EHTLPVNPETKKKIGSGACAVTQPSKRDHPCAVSDVASYHGVMSDECKAF
UY	121 KPSGVNINVTCPATNCTTTPKPKPSQACPIKCTYVVDKPKSPPEPQYPLVPQR
DB	174 KPSLVNINVTCPATNCTTTPKPKPSQACPIKCTYVVDKPKSPPEPQYPLVPQR
UY	181 SADECHCAKAKRSGHAPVPEIIPAI SPPQVITTFAPPPHVIISPASAFETAS
DB	234 SADECHCAKAKRSGHAPVPEIIPAI SPPQVITTFAPPPHVIISPASAFETAS
UY	241 MMSSTLFAIETVHMTSAKAKIPEVETSIPTQVYVIFPSWMEVIMMGTWREKID
DB	294 MMSSTLFAIETVHMTSAKAKIPEVETSIPTQVYVIFPSWMEVIMMGTWREKID
UY	301 LIFAPPIVITDPPKGVETITFPMILATTSPPPEIKDHEVYGVAMITLNSSVPI
DB	454 LIFAPPIVITDPPKGVETITFPMILATTSPPPEIKDHEVYGVAMITLNSSVPI
UY	461 VVATGADSSSKPIAHILNATVALWVAVKSSQSSQSMRANLMLSHVRASSKCR
DB	414 VVATGADSSSKPIAHILNATVALWVAVKSSQSSQSMRANLMLSHVRASSKCR
UY	421 EHTLNNKGVNVVYVITFPMI NAIYIPEVYSSITQSSSTKPEDEKPEVQSSQ
DB	474 EHTLNNKGVNVVYVITFPMI NAIYIPEVYSSITQSSSTKPEDEKPEVQSSQ
RESULT 4	
ESR2_RAI	STANDARD: PRT: 530 AA.
ID ESR2_RAI	

AC	Q52986: Q70195: Q85285: Q55015: Q55016: Q45784: Q9R185:
DI	15-JUL-1999 (Ref. 48; Created)
DI	15-JUL-1999 (Ref. 48; last sequence update)
DI	15-OCT-2001 (Ref. 40; last annotation update)
DE	Estrogen receptor beta (ER-beta).
GN	ESR2 or NP42 or EREBA.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
OX	NCBI_Taxid=10116;
FN	[1]
FC	SEQUENCE OF 46-530 FROM N.A. (ISOFORM BETA-1).
FC	STRAIN Sprague-Dawley; Tissue: Prostate;
KX	MDLINE=76234066; PubMed=8650195;
FA	Kutiper G.S.J.M., Emark E., Polio Jalilko M., Nilsson S.,
FA	Gustafsson J. A.;
ET	Cloning of a novel receptor expressed in rat prostate and ovary.*
EL	Proc. Natl. Acad. Sci. U.S.A. 93:5925-5930(1996).
FN	[2]
FC	SEQUENCE OF 46-530 FROM N.A. (ISOFORM BETA-2).
FC	STRAIN Wistar; Tissue: Ovary;
KX	MDLINE=98262942; PubMed=9600883;
FA	Mariyama K., Esch H., Sasaki Iwaka H., Kanou H., Shimaya E.,
FA	Hashimoto S., Kato S., Kawashima H.;
ET	A novel isoform of rat estrogen receptor beta with 18 amino acid
ET	insertion in the ligand binding domain as a putative dominant
EL	negative regulator of estrogen action.*
EL	Biochem. Biophys. Res. Commun. 241:142-147(1998).
FN	[3]
FC	SEQUENCE FROM N.A. (ISOFORM BETA-2).
FC	STRAIN Wistar; Tissue: Prostate;
KA	Aldridge T.C.;
ET	Tissue specific responses to estrogen: an explanation based on
ET	differential activation of multiple estrogen receptors with different
ET	estrogen response elements.*
EL	Submitted (Nov 1997) to the EMBL/GenBank/TrEMBL databases.
FN	[4]
FC	SEQUENCE OF 46-530 FROM N.A. (ISOFORMS BETA-1; BETA-2; DELTA-3).
FC	STRAIN Sprague-Dawley;
KX	MDLINE=98151095; PubMed=9492041;
FA	Petersen D.N., Tkalecovic G.T., Koza-Taylor P.B., Turf I.O.;
FA	Brown T.A.;
ET	Identification of estrogen receptor beta2, a functional variant of
ET	estrogen receptor beta expressed in normal rat tissues.*
EL	Endocrinology 139:1082-1092(1998).
FN	[5]
FC	PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1/DELTA-4).
FC	STRAIN Sprague-Dawley; Tissue: Brain;
KA	Prico R., Honda R.J.;
ET	A novel splice variant of estrogen receptor beta found in rat
ET	brain.*
EL	Submitted (Nov 1997) to the EMBL/GenBank/TrEMBL databases.
FC	FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-
FC	ALPHA. AND ACTIVATES EXPRESSION OF PRINCIPLE GENE CONTAINING
FC	ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
FC	ISOFORMS BETA-1/DELTA-3 AND BETA-2/DELTA-4 ARE UNABLE TO BIND DNA
FC	AND ACTIVATE TRANSCRIPTION DUE TO THE TRUNCATION OF THE DNA
FC	BINDING DOMAIN. ISOFORM BETA-2 SHOWS LOSS OF LIGAND BINDING
FC	AFFINITY AND SUPPRESSES ER ALPHA AND ER BETA-1 MEDIATED
FC	TRANSCRIPTIONAL ACTIVATION AND MAY ACT AS A DOMINANT NEGATIVE
FC	REGULATOR OF ESTROGEN ACTION.
FC	1
FC	SEQUENCE: BINDS DNA AS A HOMO-DIMER. CAN FORM A HETERODIMER WITH ER
FC	BETA-2.
FC	ALPHA. CAN ALSO FORM HETERODIMERS BETWEEN ISOFORMS BETA-1 AND
FC	BETA-2.
FC	1-1 SUBCELLULAR LOCATION: Nuclear.
FC	1-1 ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS: BETA-1 (SHOWN HERE),
FC	BETA-1/DELTA-3, BETA-1/DELTA-4, BETA-2, AND BETA-2/DELTA-4; ARE
FC	PRODUCED BY ALTERNATIVE SPLICING.
FC	1-1 TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, OVARY, UTERI, LIVER,
FC	KIDNEY, FAT, BONE, BRAIN, UTERUS AND TESTIS.
FC	1-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
FC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
FC	1-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.


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DR      HSP; p0437; 1HCO.
DR      InterPro: IPR000536; hormone_rec_14.
DR      InterPro: IPR01628; Zn1_4steroid.
DR      Pfam: PF0104; hormone_rec_1.

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BA	Carduaca H. hunko K.A., Hsieh R.M., Pope W.F., Mowbray K.P.: "Androgen receptor beta in the sheep ovary during the estrous cycle and early pregnancy."	21
RL	Biol. Reprod. 65:128-134(2001).	22
CC	-1- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-ALPHA, AND ACTIVATES EXPRESSION OF REPEAT GENES CONTAINING ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.	23
CC	-1- SHOWN TO BIND DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-ALPHA (BY SIMILARITY).	24
CC	-1- SUBCELLULAR LOCATION: Nuclear.	25
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: BETA (SHOWN HERE) AND BETA-1. ARE PRODUCED BY ALTERNATE SPLICING.	26
CC	1. DOMAIN: COMPOSED OF THREE DOMAINS, A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	27
CC	-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.	28
CC	NR3 SUBFAMILY.	29
CC	-----	30
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CC	EMBL: AF179316; AN55772.1; -	32
DR	EMBL: AE57109; AAF7145.1; -	33
DR	HSSP: P03472; IHCO.	34
DR	InterPro: IPR000546; hormone_rec_1q.	35
DR	InterPro: IPR001723; Steroid_receptor.	36
DR	InterPro: IPR001648; Zn1_Cstereoid.	37
DR	pfam: PF00104; hormone_rec_1.	38
DR	pfam: PF00105; z1-c4_1.	39
DR	PRINTS: PR00398; STEROHORMER.	40
DR	PRINTS: PR00047; STEROIDFINDER.	41
DR	ProDom: PD000045; Zn1_Cstereoid_1.	42
DR	SMART: SM00430; R01.1; 1.	43
DR	SMART: SM00399; ZN_C4_1; 1.	44
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR_1.	45
DR	Receptor: Transcription regulation: DNA-binding; Nuclear protein; DNA-binding; Steroid binding; Alternative splicing; Phosphorylation.	46
FW	1. 145	47
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FW	1. 145	133
FW	1. 145	134
FW	1. 145	135
FW	1. 145	136
FW	1. 145	137
FW	1. 145	138


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UY 441 MMSSTKLADKELVIMHSMARKIPGVELSLTQVRLLESWLEVLAMLMKMSLDHCK 470
    |||||||
DB 471 MMSSTKLADKELVIMHSMARKIPGVELSLTQVRLLESWLEVLAMLMKMSLDHCK 450
    |||||||
UY 451 LITAPDVLDRDCKVEGILEPMLATTSPREKLQREYLVKAMILLNSMYPL 460
    |||||||
DB 451 LITAPDVLDRDCKVEGILEPMLATTSPREKLQREYLVKAMILLNSMYPL 410
    |||||||
UY 461 VTAIGVDSPPKRAHNAVITAWVLAKSSISSQSMPLANLMLSHVIRASNGM 420
    |||||||
DB 411 AIDVAFDSSKRELLIMNAVITAWVLAKSSISSQSMPLANLMLSHVIRASNGM 470
    |||||||
UY 421 EHLNKKKNVAVVYLLLEMLNAVVLKSSISSQSMPLANLMLSHVIRASNGM 477
    |||||||
DB 471 EHLNKKKNVAVVYLLLEMLNAVVLKSSISSQSMPLANLMLSHVIRASNGM 527
    |||||||

RESULT 7
ESR2_P10: STANDARD: PRT: 526 AA.
AC GXXSW2: GYHAW5:
IT 16 OCT 2001 (rel. 40, created)
IT 15 JUN 2002 (rel. 41, last sequence update)
IT 15 JUN 2002 (rel. 41, last annotation update)
DE Estrogen receptor beta (Erb beta)
GN ESR2 OR NR1A2.
OS Steroid (P10).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI Taxid 9825.
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: Embryo;
RA Kowalski A.A., Graddy L.G., Valle-Cruz D.S., Choi L.,
    Katzenellenbogen B.S., Shimen P.A., Shimen R.C.M.;
RT "Molecular cloning of porcine estrogen receptor beta cDNAs and
    developmental expression in post implantation embryos."
RL Submitted (Jun. 2001) to the EMBL/Genbank/DBS databases.
RN 121
RP SEQUENCE FROM N.A.
RC TISSUE: ovary;
RA Lavoie H.A., Desjardins D.C.;
RT "Cloning and expression of estrogen receptor beta isoforms from
    porcine ovary."
RL Submitted (Mar. 2001) to the EMBL/Genbank/DBS databases.
AC FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
    ER ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
    ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN DEPENDENT MANNER.
CC SUBMITTER BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER
    ALPHA (BY SIMILARITY).
CC SUBCELLULAR LOCATION: Nucleus.
CC DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
    A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
CC SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
    NR3 SUPERFAMILY.

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or send an email to license@isb.sib.ch).

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EN 2102 Erythrocyte Steroid Binding, Phosphorylation.
PT DOMAIN 1 145 MODULATING.
PT DOMAIN 146 211 NUCLEAR RECEPTOR TYPE.
PT ZN_F1085 146 166 C4-TYPE.
PT ZN_F1085 162 206 C4-TYPE.
PT DOMAIN 212 526 STEROID-BINDING (BY SIMILARITY).
PT M02_PES 84 84 PHOSPHORYLATION (BY SIMILARITY).
PT M02_PES 484 484 PHOSPHORYLATION (BY SIMILARITY).
PT CONFLICT 417 417 M - V (IN REF. 2).
PT CONFLICT 469 469 T - M (IN REF. 2).
SC SEQUENCE 526 AA: 58849 MW: 55020 Da: 1078886 C664.

Query Match: 86.4%; Score 2380; DB 1; Length 526;
Best local similarity: 86.4%; Prod. No. 3-20-172;
Matches: 412; Coverage: 26; Mismatches: 65; Indels: 4; Gaps: 2;

UY 1 MMSSTKLADKELVIMHSMARKIPGVELSLTQVRLLESWLEVLAMLMKMSLDHCK 60
    |||||||
DB 54 VNYSTSS---NSFVGRQATSPNVLWPHSHSLAHQUSLYARQKSPWDRSL 110
    |||||||
UY 61 EHLNKKKNVAVVYLLLEMLNAVVLKSSISSQSMPLANLMLSHVIRASNGM 120
    |||||||
DB 111 EHLNKKKNVAVVYLLLEMLNAVVLKSSISSQSMPLANLMLSHVIRASNGM 170
    |||||||
UY 121 MMSSTKLADKELVIMHSMARKIPGVELSLTQVRLLESWLEVLAMLMKMSLDHCK 180
    |||||||
DB 171 KRSYGHINYLCHVATNCTTIRKRRKSVQVCHLRKCYGVCKVSRREKGYRVRKOR 240
    |||||||
UY 181 SAEQYHFAKAKRSGHNPVRRLLDALSPQVITLLFAEPHYLLSPSPAPTFAS 240
    |||||||
DB 231 NSHAEHFLSKAKRRSHHTKVELLSLTSQVITLLFAEPHYLLSPSPAPTFAS 290
    |||||||
UY 241 MMSSTKLADKELVIMHSMARKIPGVELSLTQVRLLESWLEVLAMLMKMSLDHCK 300
    |||||||
DB 291 MMSSTKLADKELVIMHSMARKIPGVELSLTQVRLLESWLEVLAMLMKMSLDHCK 350
    |||||||
UY 401 LITAPDVLDRDCKVEGILEPMLATTSPREKLQREYLVKAMILLNSMYPL 360
    |||||||
DB 451 LITAPDVLDRDCKVEGILEPMLATTSPREKLQREYLVKAMILLNSMYPL 409
    |||||||
UY 461 VTAIGVDSPPKRAHNAVITAWVLAKSSISSQSMPLANLMLSHVIRASNGM 420
    |||||||
DB 410 SAAQVFAESSKRELLIMNAVITAWVLAKSSISSQSMPLANLMLSHVIRASNGM 469
    |||||||

RESULT 8
ESR2_STUDV: STANDARD: PRT: 554 AA.
AC GYVEE2:
IT 16 OCT 2001 (rel. 40, created)
IT 16 OCT 2001 (rel. 40, last sequence update)
IT 16 OCT 2001 (rel. 40, last annotation update)
DE Estrogen receptor beta (Erb beta)
GN ESR2 OR NR1A2.
OS Steroid vulgaris (Starling).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Actinopterygii; Atheri; Neuplatycten; Steniodon; Steniodon.
OX NCBI Taxid 9172.
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: Brain;
RA MEDLINE 99427866; PubMed 10499520;
    Reinhard D.L., Bentley G.E., Ballhazart J., Furck P.W., Ball G.F.;
RT "Androgen receptor, estrogen receptor alpha, and estrogen receptor
    beta show distinct patterns of expression in bovine brain control
    and after treatment with androgens."
RL Endocrinology 140:4644-4644(1999).
CC FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER
    ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING

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[illegible]

DE PRINTS: PR000476, STEROID-BINDING.
 DE SMART: SM00430; H0L1: 1.
 DE PROSITE: PR000476; NUCLEAR RECEPTOR: VARIAT.
 KW Receptor, Transcription regulation, DNA binding, Nuclear protein.
 KW Zinc finger, Steroid binding, Phosphorylation.
 FT NUC TER 1
 FT DOMAIN 1 279
 FT PRO BIND 251
 FT NUC TER 279
 FT NUC TER 279
 SEQUENCE 279 AA: 8581987D01DAB01 CR664:

Query Match 55.48; Score 1498; DB 1; Length 279;
 Best Local Similarity 98.78; Pred. No. 4; 50-100;
 Matches 274; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DB 185 QIARACKRSGSHARVRELLDALSPQVATLLEADPRVILLSPQAPETASMMMS 244
 |||
 DB 1 QIARACKRSGSHARVRELLDALSPQVATLLEADPRVILLSPQAPETASMMMS 60
 245 LTRAKRELVHMLSMARKTRGVETSLRQVYLLSSQWMEVLMKGLMMKSLDREKELTA 304
 |||
 DB 61 LTRAKRELVHMLSMARKTRGVETSLRQVYLLSSQWMEVLMKGLMMKSLDREKELTA 120
 405 POLVILDRDREKVEGILLTFPDLATTSREKELKQREKYLGVKAMILLNSMTLVAT 364
 |||
 DB 121 POLVILDRDREKVEGILLTFPDLATTSREKELKQREKYLGVKAMILLNSMTLVAT 180
 465 QIARACKRSGSHARVRELLDALSPQVATLLEADPRVILLSPQAPETASMMMS 424
 |||
 DB 181 QIARACKRSGSHARVRELLDALSPQVATLLEADPRVILLSPQAPETASMMMS 240
 425 NMGRKNVYVYDILLMLNAHVLRKSSITSESPAR 463
 |||
 DB 241 NMGRKNVYVYDILLMLNAHVLRKSSITSESPAR 279

RESULT 13

ESR1 CANAD
 ID ESR1 CANAD STANDARD; PRT: 568 AA.

DE 16-OCT 2001 (Ref. 40, created)
 DE 16-OCT 2001 (Ref. 40, last sequence update)
 DE 15-JUN 2002 (Ref. 41, last annotation update)
 DE ESTROGEN RECEPTOR BETA 1 (ER beta-1).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 NX NBTX ID: 7957;
 RN 111
 RP SEQUENCE FROM N.A.
 RS TISSUE: Liver.
 RX MEDLINE 99161177; PubMed 10068500;
 RA Tikhonova A.V.; Pathak S.; Falande J.V.;
 RT "Molecular cloning of an estrogen receptor beta subtype from the
 RT goldfish, *Carassius auratus*."
 RL Gen. Comp. Endocrinol. 113:488-490(1999).
 RL 1- FUNCTION: HINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 ER ALPHA, AND ACTIVATES EXPRESSION OF RECEPTOR GENES CONTAINING
 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN DEPENDENT MANNER.
 1- SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER
 ALPHA (BY SIMILARITY).
 1- SUBCELLULAR LOCATION: Nucleus.
 1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
 1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 NC1 SIMILARITY.

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 or send an email to license@ebi.ac.uk.

DE ESR1: A061269; A026921; 1.
 DE HSSP: P04372; ERK.
 DE 16-OCT 2001 (Ref. 40; Hormone rec 119.
 DE 16-OCT 2001 (Ref. 40; Hormone rec 119.
 DE 16-OCT 2001 (Ref. 40; Hormone rec 119.
 DE 16-OCT 2001 (Ref. 40; Hormone rec 119.
 DE PRINTS: PR000476, STEROID-BINDING.
 DE SMART: SM00430; H0L1: 1.
 DE PROSITE: PR000476; NUCLEAR RECEPTOR: VARIAT.
 KW Receptor, Transcription regulation, DNA binding, Nuclear protein.
 KW Zinc finger, Steroid binding, Phosphorylation.
 FT NUC TER 1
 FT DOMAIN 1 279
 FT PRO BIND 251
 FT NUC TER 279
 FT NUC TER 279
 SEQUENCE 279 AA: 8581987D01DAB01 CR664:

Query Match 55.08; Score 1386; DB 1; Length 568;
 Best Local Similarity 58.78; Pred. No. 1; 10-100;
 Matches 269; Conservative 65; Mismatches 104; Indels 20; Gaps 7;

DB 18 ROTTENNVNLTGHSPLVHROLSHYA-EPOKSPWFAKSLPHTLVNKKKVS 76
 |||
 DB 93 ROTTENNVNLTGHSPLVHROLSHYA-EPOKSPWFAKSLPHTLVNKKKVS 152
 77 GNRCAVVTGSGRIARFVAVCSYASVYHGVMS-DEKAKFKRSYUQINQY 146
 |||
 DB 153 VARETS-SLRKADIMHGVAVSIVASVYHGVMS-DEKAKFKRSYUQINQY 210
 147 GNRCAVVTGSGRIARFVAVCSYASVYHGVMS-DEKAKFKRSYUQINQY 194
 |||
 DB 211 GNRCAVVTGSGRIARFVAVCSYASVYHGVMS-DEKAKFKRSYUQINQY 266
 195 SRCAVVR-----ELLDALSPQVATLLEADPRVILLSPQAPETASMMMS 244
 |||
 DB 267 SRCAVVR-----ELLDALSPQVATLLEADPRVILLSPQAPETASMMMS 426
 245 LTRAKRELVHMLSMARKTRGVETSLRQVYLLSSQWMEVLMKGLMMKSLDREKELTA 404
 |||
 DB 527 LTRAKRELVHMLSMARKTRGVETSLRQVYLLSSQWMEVLMKGLMMKSLDREKELTA 486
 405 POLVILDRDREKVEGILLTFPDLATTSREKELKQREKYLGVKAMILLNSMTLVAT 363
 |||
 DB 487 POLVILDRDREKVEGILLTFPDLATTSREKELKQREKYLGVKAMILLNSMTLVAT 446
 444 TETACSSPEALINAVTALVAVSIVASVYHGVMS-DEKAKFKRSYUQINQY 423
 |||
 DB 447 GNRCAVVTGSGRIARFVAVCSYASVYHGVMS-DEKAKFKRSYUQINQY 506
 424 LNRKNVYVYDILLMLNAHVLRKSSITSESPAR 463
 |||
 DB 507 LNRKNVYVYDILLMLNAHVLRKSSITSESPAR 544

RESULT 14

ESR2 CANAD
 ID ESR2 CANAD STANDARD; PRT: 568 AA.

DE 16-OCT 2001 (Ref. 40, created)
 DE 16-OCT 2001 (Ref. 40, last sequence update)
 DE 16-OCT 2001 (Ref. 40, last annotation update)
 DE ESTROGEN RECEPTOR BETA 1 (ER beta-1).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.


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06 NBI_Laxid 8022:
07
08
09 SEQUENCE FROM N.A.
10 Head M. Acetone-2, 4, 6, 8
11 Molecular cloning of an estrogen receptor beta subtype from rainbow
12 trout.
13 Submitted (01-2000) to the EMBL/Genbank/DDBJ databases.
14
15 FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
16 ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
17 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
18
19 SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-
20 ALPHA (BY SIMILARITY).
21
22 SUBCELLULAR LOCATION: Nuclear.
23
24 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
25
26 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
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456 RLLNATVIALVMAISRTGISTQVSAPIAHMLSHIPHLNPMTHHSSMKNVYV 516
 455 YLLLEMLNAHVE: RCKSSITQSESPA 462
 516 YLLLEMLNANMAQSHVSTVCTDPTPA 545

RESULT 17
 ERR2_CARAU STANDARD: PRT: 610 AA.
 AC 091A19;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE Estrogen receptor beta-2 (EP-beta-2)
 DE Carassius auratus (Goldfish)
 DE Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi:
 DE Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes:
 DE Cyprinidae: Carassius.
 NC Nhl_TaxID:7957;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE: Brain, and pituitary;
 RX MEDLINE:20246301; PubMed 10786629;
 RA Ma C.H., Dong K.W., Yu K.L.;
 RT cDNA cloning and expression of a novel estrogen receptor beta-subtype
 in goldfish (*Carassius auratus*).
 RL Biochem. Biophys. Acta 1490:145-152(2000).
 CC 1 FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
 CC SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 ALPHA (BY SIMILARITY).
 CC 1-1 SUBCELLULAR LOCATION: Nuclear.
 CC 1-1 TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN PITUITARY.
 CC 1-1 TELECEPHALON AND HYPOTHALAMUS AS WELL AS IN THE LIVER.
 CC 1-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC 1-1 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC 1-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see: <http://www.isb.ch/protomol/>
 CC or send an email to license@isb.ch).
 CC -----

DR EMBL: AF17465; AAF170 1;
 DR HSSP: P03372; HRC;
 DR InterPro: IPR000536; Hormone_rec_119;
 DR InterPro: IPR001723; Steroid_receptor;
 DR InterPro: IPR001628; Zn1_C4steroid;
 DR Pfam: PF00104; hormone_rec_1;
 DR Pfam: PF00105; z1-c4_1;
 DR PRINTS: PR00348; STEROHORMNER;
 DR PRINTS: PR00047; STEROIDFNGR;
 DR ProDom: PD000035; Zn1_C4steroid_1;
 DR SMART: SM00430; H011; 1;
 DR SMART: SM00399; Zn1_C4_1;
 DR PROSITE: PS00041; NUCLEAR_RECEPTOR_1;
 DR PROSITE: PS00041; NUCLEAR_RECEPTOR_1;
 KW Receptor; Transcription regulation; DNA binding; Nuclear protein;
 KW Zinc-finger; Steroid binding
 FT DNAME 1 170 MODULATING;
 FT DNAME_BIND 171 246 NUCLEAR RECEPTOR TYPE;
 FT ZN_FING 171 191 C4 TYPE;
 FT ZN_FING 207 241 C4 TYPE;
 FT DNAME 237 588 STEROID-BINDING;
 FT SEQUENCE 610 AA; 67851 MW; 029F2CFC16C67 CRC64;

Query Match: 52.7%; Score 1328; DR 1; Length 610;
 Best Local Similarity: 57.5%; Pctd. Id.: 56.10%;

Matches: 277; Conserved: 61; Mismatches: 199; Gaps: 52; Gaps: 9;
 25 VLMPF-PGHL-----SPLVVKHLSHLYAFQKSPWLEAKS-LEHTLVNRELRKKV 75
 96 LMPHPHSTDSI HCPSPFLAYRPHHATHTWDAKTHINGSSVITIA - -KIDGOL 150
 76 SGNPVSPTVGSKDAHFRVAVCSIVASGIRYVWSCGCKAPFKKSGHNYITAT 135
 151 LQGLNLPSPGKIDHFRCAVCHDYSAGHYVWSCGCKAPFKKSGHNYITAT 210
 136 NQPTLNKPKSQAQCHKCYFVWVKQSSPPRCYPIVWPSASAPQ HCKAKPS 195
 213 MCTTLESPPRSQVLEKCELEVEMKCVRRHSSTFGRRHNPRL ESYVALGV 269
 196 GSHAPPELLIA-----LSPQVTLFAHPIHLSPI-SAPET 247
 270 KQSHQILTEPLSTFHTFGLHKAQVQGNLSFGVNLHATPGYLRHLEKRYT 329
 238 EASMMSLTKLAKELVHMSNAKKIPEVVELSLDQVKLESTMEVLMMLKSLDH 297
 330 EASMMSLTNIAKELVHMSNAKKIPEVVELSLDQVKLESTMEVLMMLKSLDH 389
 298 PEKTIAPAPVVIPEPKGVPELLEPIPMIATTSPPEPKIQRKPYIVKAMII NSM 357
 390 PEKTIAPAPVVIPEPKGVPELLEPIPMIATTSPPEPKIQRKPYIVKAMII NSM 449
 458 YPLVAT-GDANSSKRLAHNLNAVTDALVWIAKSGISSQGSRIANLMLSHVRIAS 416
 450 GSRVQVDFPVESKQVLEKLSVIALVWISKISLSSHOSSIKADMLMLSHVRIAS 509
 417 NQMTHEHMMKKNVAVVILLMLNAHVIKGNSSIIQSPS----- 460
 510 NQMTHEHMMKKNVAVVILLMLNAHVIKGNSSIIQSPS----- 460
 461 --PAVNSKSPSSQNPQSSQ 477
 570 QQPALESNDPFRSHQAE 588

RESULT 18
 ERR2_SPAU STANDARD: PRT: 559 AA.
 AC 09W6M2;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE Estrogen receptor beta-2 (EP-beta-2)
 DE Carassius auratus (Goldfish)
 DE Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi:
 DE Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes:
 DE Cyprinidae: Carassius.
 NC Nhl_TaxID:8175;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE: Ovary;
 RA SNOTTO S., Power D.M., Olsson P.-E., Canario A.V.M.;
 RT Two estrogen receptors expressed in teleost fish: cDNA cloning,
 RT characterization and tissue distribution.
 RL submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC 1-1 FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
 CC 1-1 SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 ALPHA (BY SIMILARITY).
 CC 1-1 SUBCELLULAR LOCATION: Nuclear.
 CC 1-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC 1-1 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC 1-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.

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	Quercy Match	Forest Local Stimulativity	Matchos 259; Conservative
Score	1322.5;	508.1;	577;
Length	5599;	150-101;	Indels 15;
Ops	6;		

[illegible]

RESULT 19		
ESR4	MITON	PPT:
AT	ESR4 MITON	565, AA.
AD	P572H33	
DT	16 OCT 2001 (bel. 40, Cited-as)	
DT	16 OCT 2001 (bel. 40, last sequence update)	
DT	16 OCT 2001 (bel. 40, last annotation update)	
DE	ESTR40R, PPT-047, gamma (Efr gamma)	
DN	ESR4 FOR NR 43	

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139	EMBL: AF09182; AAC16712.1; -
139	HSSP: P03472; 1E8R.
139	InterPro: IPRO00546; Hormone_Rec_14.
139	InterPro: IPRO01724; Steroid_Receptor.
139	InterPro: IPRO01628; Znf_C4steroid.
139	PIfam: PF00104; hormone_Rec_1.
139	PIfam: PF00105; Zf_C4_1.
139	PRINTS: PR00498; STEROIDOMER.
139	PRINTS: PR00472; STEROIDINGER.
139	Prodom: PRO00045; Znf_C4steroid_1.
139	SMART: SM00410; HOL1_1.
139	SMART: SM00399; ZNF_C4_1.
139	PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
139	Receptor; Transcription regulation; DNA binding; Nuclear protein;
139	MM zinc-finger; Steroid binding.
139	DOMAIN 1 168 MODULATING.
139	DOMAIN 169 234 NUCLEAR RECEPTOR TYPE.
139	ZN_F1363 169 189 C4 TYPE.
139	ZN_F1363 205 229 C4 TYPE.
139	DOMAIN 235 285 HINC.
139	DOMAIN 286 520 STEROID-BINDING.
139	SEQUENCE: 565 AA; 6290 k MW; D995412P74007A56; C1664;

[illegible]

[illegible]

- 447 SLHGVLLTSSMLFVLMIGLWRSLOFGKLLFPAQDILLDRNGCEVEGMALFDMLLA (48)
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 450 TTPSPPTKDKRPVGVKMMTLLSSMPLVTAQD ANSSRKALHLLNAVTAQVVI (49)
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 457 TAPSPKIKIKIEEPVETKALLTNSGASPTGTEPPLHSAVAQIMLDITVILL (44)
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PRIN1: PR00047: STEROIDRECEPTOR.
DR PROTEIN: PD000035; ZNF_C4steroid; 1.
DR SMART: SM00430; HOL1; 1.
DR SMART: SM00399; ZNF_C4; 1.
DR PROSITE: PS00041: NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein.
KW Zinc-finger; Steroid-binding; MODULATING.
FT DOMAIN 1 179 MODULATING.
FT DNABIND 180 245 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 180 200 C4-TYPE.
FT ZN_FING 216 240 C4-TYPE.
FT DOMAIN 246 302 HINGE.
FT DOMAIN 303 586 STEROID-BINDING.
SU SEQUENCE 586 AA: 66080 MM: 080677ER006P08BF CR064:

Query Mapch 47 69: Score 1199.5; DR 1; Length 596;
Best local similarity 52.0%; Pred. No. 2.8e-91;
Matches 24; Conservative 76; Mismatches 117; Gaps 9;

DY 22 SPVAVMTPTPLSLPTVVR-QLSHYAPPLKPSWCFARSLHTLTVNPTLKKYSGNKG 80
DB 101 SPVPLAKLPDLPSPFHHHQVYVLESQVTFVAFAPAPTF-YRSSINRPGSGPFP 159
DY 81 ASPVTPPT-----SKPLAFCAV-SDYASAYGCVMSGEGCAPEKSTGCHRYCTPAT 135
DB 150 MSSANIKGKPSMSTAFVYAV-SYVASYDHYGVMSDEGCAPEKSTGCHRYCTPAT 219
DY 146 NGTTTTPNPKS-QN-PLP-YV-VNVR-TSEPTT-YVPTVFEGSALFEG-NVA-YVAF 195
DB 220 NGCTTTPNPKS-QN-PLP-YV-VNVR-TSEPTT-YVPTVFEGSALFEG-NVA-YVAF 274
DY 196 GCHV-----PPVPELIDP-----ALSPQVLTLEAPPHVLTSPPA-PPFPASM 241
DB 275 VETSTTASTVWNP-VKSKTSLAFQSLAMKAPATVSTSGS-TPQ-STAVM 444
DY 242 MMSLTAKLCKELVHMTSMARKTNGVELSLFDQVRLTSCMNVLMKGMMSLHPTSKL 401
DB 335 MTLINLADRELHVMIMARKVGVDTLHQVHLFQAMLEFLMVLIMBSVHPCKL 494
DY 302 IFAPDVLDRDEKCVKSLLEIFDMLATTSPREKLQHKYLCVKAMILLNSKMYLV 361
DB 395 SFANLILDRNCPQVYVETFTMTVTATFETKMPFEEELVTFETLINSVET 454
DY 362 TATQDAUSKRLAH-LINAVTALVWIAKSGSSQSGMRANLMLLSHVHAKNKM 420
DB 455 SLLTSTPTPTLHTLHPKTPPTVHFMKASQSLGQQLPPLAQTLTSHLPMNSPM 511
DY 421 EHLNKKCKNVVYVDLLEMLNAVLKCKSSITGSGSPADSKS 467
DB 515 EHYMKCKNVVPLDILLEMLAHPTTKTKTKTTF-----PDSGS 557

RESULT 27
ESRL_MOUSE STANDARD: PRT: 599 AA.
AC P19785; Q9QY51; Q9QY52;
DI 01-FEB-1991 (Rel. 17, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Estrogen receptor (ER) (Estrogen receptor) (ER-alpha).
DS ESTR OR NR3A1 OR ESR OR ESRB OR ESRP
DS Mus musculus (Mouse).
DS Eukaryotic; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;
DS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OS NCBI_TaxID=10090;
RN 111
RS SEQUENCE FROM N.A.
RC TISSUE: uterus;
RA MEDLINE=91042558; PubMed=2484714;
RA White R., Lewis J.A., Needham M., Han T., Parker M.;
RT "Structural organization and expression of the mouse estrogen
receptor";
RL Mol. Endocrinol. 15:735-744(1987).

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KN 121
KN SEQUENCE OF 269-599 FROM N.A.
KN SPAIN-ST/71; and R10 S/71; TISSUE: Spleen;
KN Ma R.Z., Teuscher G.;
KN "Screening for candidate genes of mouse autoimmune diseases";
KN selected (Jan 1999) to the FMI/Genbank/DBM databases.
KN [3]
KN CARBOHYDRATE-LINKAGE SITE SER-575.
KN MEDLINE=97153020; PubMed=8999954;
KN Jiang M.S., Hart G.W.;
KN "A subpopulation of estrogen receptors are modified by O-linked
KN N-acetylglucosamine";
KN J. Biol. Chem. 272:2421-2426(1997).
KN [4]
KN CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575.
KN MEDLINE=2124187; PubMed=11256841;
KN Cheng X., Hart G.W.;
KN "O-glycosylation of the murine estrogen receptor-alpha";
KN J. Steroid Biochem. Mol. Biol. 75:147-158(2000).
KN 1. FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
KN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
KN PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
KN 2. SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
KN BETA (BY SIMILARITY).
KN 3. SUBCELLULAR LOCATION: Nuclear.
KN 4. DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
KN A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
KN 5. TTR: PHOSPHORYLATED BY CYCLIN A/CYCL2 (BY SIMILARITY).
KN 6. MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS
KN ARE BELIEVED TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;
KN HORMONE-BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE
KN HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISPERSED DNA
KN SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.
KN 7. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
KN NR3 SUBFAMILY.
KN -----
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KN entities requires a license agreement (see http://www.isb-sib.ch/aboutus/
KN or send an email to license@isb-sib.ch).
KN -----
KN EMBL: M36651; AAA37580.1; --
KN EMBL: A0128231; AAF22562.1; --
KN EMBL: A0128230; AAF22561.1; --
KN PIR: A40061; A40061.
KN HSSP: P03372; HSCP.
KN TRANSFAC: T00259; --
KN GLYCOSULEDB: P19785; --
KN MDJ: M011352467; ESRL.
KN InterPro: IPK000536; Hormone_rec_14.
KN InterPro: IPK001292; Oestrgn_receptor.
KN InterPro: IPK001724; Sterhmo_receptor.
KN InterPro: IPK001628; Znf_C4steroid.
KN Pfam: PF00104; hormone_rec_1.
KN Pfam: PF00105; zf-C4; 1.
KN Pfam: PF02159; Oest_recpt_1.
KN PRINTS: PR000478; STRIDHOMNER.
KN PROSITE: PS000435; ZNF_C4steroid.
KN PROSITE: PS000435; ZNF_C4steroid; 1.
KN SMART: SM00430; HOL1; 1.
KN SMART: SM00399; ZNF_C4; 1.
KN PROSITE: PS00041; NUCLEAR_RECEPTOR; 1.
KN Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KN Zinc-finger; Steroid-binding; MODULATING;
KN DOMAIN 1 188
KN DNABIND 189 254 NUCLEAR RECEPTOR-TYPE.
KN ZN_FING 189 209 C4-TYPE.
KN ZN_FING 225 249 C4-TYPE.
KN DOMAIN 255 514 HINGE.
KN DOMAIN 515 599 STEROID-BINDING.

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EN	[1]	SEQUENCE FROM N.A.
KD		TISSUE LIVER:
RX	MIMUNE 99404495; PubMed 1076207;	
KA	Menozzi et al., J. A., Jorgensen et al., Kato et al., Valdes-Ay., Gagliardi P. ;	
RI	"Cloning and sequencing of the qtl/broad sea brown estrogen receptor cDNA".	
KL	JNA Soc., 10:75-84(1999).	
KD	[2]	
KD	SEQUENCE OF 5'2 579 FROM N.A.	
RD	TISSUE LIVER:	
RX	PubMed 10927619;	
KA	Sacotto S., Power D.M., Olsson P.E., Canario A.V.M.;	
RI	"cRNA cloning and tissue expression of the qtl/broad sea brown, Sparus aurata;	
KT	aurata, estrogen receptor.";	
KL	Submitted (JUL-1997) to the EMBL/Genbank/Joint databases.	
CC	-1- POSITION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN	
CC	THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND APPROPRIATE CELLULAR	
CC	PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.	
CC	-1- SUBJECT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER	
CC	BETA (BY SIMILARITY).	
CC	-1- SUBCELLULAR LOCATION: Nuclear,	
CC	-1- DOMAIN: COMPOSED OF THREE DOMAINS: A MEDIATING N-TERMINAL DOMAIN,	
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	
CC	-1- SIMILARITY: RELATES TO THE NOBLEAP HORMONE PROTEIN FAMILY.	
CC	NK3 SUPERFAMILY.	
CC		
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CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed, usage by and for commercial	
CC	entities requires a license agreement (see http://www.isb.ac.uk/journals/stb/ch).	
CC	or send an email to licenses@sb.stb.ch).	
DK	EMBL: A0006339; CAB51479.1;	
DK	EMBL: AF106779; AB041032.1;	
DK	EMBL: AF014104; AA082428.1;	
DK	ECSF 19337.2; IBER.	
DK	HeteroPro: IPRO00546; Hormone rec 13q.	
DK	HeteroPro: IPRO01723; Steroid receptor.	
DK	HeteroPro: IPRO01628; ZnfC4Steroid.	
DK	Pfam: PF00104; hormone_rec1_1.	
DK	Pfam: PF00105; z1-C4_1.	
DK	PRINTS: PR00396; STIMHORMONR.	
DK	PRINTS: PR00047; STEROIDEPTNCR.	
DK	ProDom: PR00045; Znf_C4Steroid; 1.	
DK	SMART: SM00430; BDL1; 1.	
DK	SMART: SM00599; ZNF_C4; 1.	
DK	PROSITE: PS00341; NOBLEAK_RECEPTOR; 1.	
KW	Receptor, Transcription regulator; DNA binding; Nuclear protein;	
KW	Zinc finger, Steroid binding.	
F1	DOMAIN 1 142	
F1	DNA_BIND 141 208 MODULATING (BY SIMILARITY);	
F1	ZN_FING 141 163 NUCLEAR RECEPTOR-TYPE.	
F1	ZN_FING 179 203 C4-TYPE.	
F1	DOMAIN 209 270 HINCH.	
F1	DOMAIN 271 579 STEROID-BINDING (BY SIMILARITY);	
F1	DOMAIN 259 263 POLY GLY.	
F1	DOMAIN 533 537 POLY SER.	
F1	DOMAIN 533 543 POLY GLY.	
F1	CONFLICT 83 86 OPAK -> HPPK (IN REF. 2).	
F1	CONFLICT 98 98 Y -> YES (IN REF. 2).	
F1	CONFLICT 480 480 K -> N (IN REF. 5).	
SD	SOURCE 579 AA; b3361 MW; 7B91A7AA96471E chr64;	

443 NAAVLKCKSSITGSCFAPADSKSE 469
DB 545 DAHRLH-APNLG---PPEEDMSQ 567

RESULT 31
ESRL_HORSE
ID ESRL_HORSE STANDARD: PRT: 620 AA
AC P50241:
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-OCT-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estradiol receptor (ER) (Estradiol receptor) (ER-alpha).
DS ER OR NR3A1 OR MER.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Actinopterygii; Perciformes; Atherinomorpha;
OC Helostomus; Adrianchthyidae; Oryziatidae; Oryzias
OX NCBI_TaxId=8090;
X 111
RF SEQUENCE FROM N.A.
RA STRAIN-D-R: J1SS0F Liver;
RA Osaka H., Kawahara T., Yamashita T.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases
RN 121
RP SEQUENCE FROM N.A.
RA Kawahara T., Yamashita T.;
RF Oryzias latipes genomic DNA for estradiol receptor
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
CS 1-1 FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CS THE REGULATION OF ENDOCRINE GENE EXPRESSION AND AFFECT CELLULAR
CS PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES
CS 1-1 SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CS BETA (BY SIMILARITY).
CS 1-1 SUBCELLULAR LOCATION: Nuclear.
CS 1-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN
CS A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CS 1-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CS NR3 SUBFAMILY.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/annoucy/>
CC or send an email to license@isb-sib.ch).
CC -----

DB EMBL: D28954; BAA25900.1;
DB EMBL: AH03491; BAA86925.1;
DB HSSP: P03372; 1ERR
DB InterPro: IPR000536; Hormone_rec_11q
DB InterPro: IPR001292; Gestrin_receptor
DB InterPro: IPR001723; Steroid_receptor
DB InterPro: IPR001628; Znf_C4steroid
DB Pfam: PF00104; hormone_rec_1
DB Pfam: PF00105; z1-C4_1
DB Pfam: PF02159; Gestr_recep_1
DB PRINTS: PR00398; STROIDRENER
DB PRINTS: PR00047; STROIDRENER
DB PRODOM: PD000035; Znf_C4steroid_1
DB SMART: SM00430; HOL1_1
DB SMART: SM00399; ZNF_C4_1
DB PROSITE: PS00031; NUCLEAR_RECEPTOR_1
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding;
FT 1 185
FT DNABIND 186 251 MODULATING;
FT 2N-FING 186 206 NUCLEAR RECEPTOR TYPE;
FT 2N-FING 222 246 C4 TYPE;
FT 2N-FING 252 314 HINGE;
FT 1 252 314

FT 1 415 620
FT DOMAIN 299 407 STEROID BINDING;
FT 1 420 515 POLY-GLY;
FT 1 515 579 POLY-LEU;
FT 1 579 620 POLY-GLY;
SU SEQUENCE 620 AA; 67729 MW; DDCDHDHC2HMA522 CR664;

Query Match 47.38; Score 1192; E-Val 1; Length 620;
Post Local Similarity 49.58; Prod. No. 1,3e+90;
Matches 260; Conservative 74; Mismatches 121; Indels 70; Gaps 14;

QY 3 YSIF-----SANTLEASFGRTSPTNLTMTFSGHSPLYVHEDSHLYVAPKSP 53
RB 88 YSAPLITNPSPSGISGSP-----ISPLVYVSSRSLSPDM--HPSHHYLETSTP 141
QY 54 WCRASLEHTLPVNRFTLKKVSGNP--CASPVTPGSG-----KKDAHFAVCSQYA 103
RB 142 VVSS-----HGCASPRFQ--GSPFDQ--SGHGAZGA--AFEMAKITFCAVCSQYA 193
QY 104 SSVHGVWSFGGKAFKRSIGHNDYIGPATNCTDICKNPKSGAGLEKGVGVGVK 163
RB 194 SSVHGVWSGEGKAFKRSIGHNDYIGPATNCTDICKNPKSGAGLEKGVGVGVK 253
QY 164 CSPPRECVRELVPGP-----SALQDHPACFKKPS--GCHAPVVFPI 207
RB 254 GYVPRP--LPLPKVPRGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 311
QY 208 DALSPGVTLTAPPHVITSP--SAPFPAKMSKIVTAPFVIMKSMARKTPG 265
RB 312 ISLPPVLTITGAPV--ISLPPVLTITGAPV--ISLPPVLTITGAPV--ISLPPVLTITGAPV 370
QY 266 FVELSTFQVLLSPGMEVIMGLMSPVDFHCFIENHVALTPPVKCVPTTETP 325
RB 371 FVLSLTPVYITLPSWITVIMGLMSPVDFHCFIENHVALTPPVKCVPTTETP 430
QY 326 MLATTSPEELKREKLYKAMLLNNSVPIVATQ--AUSKRIALLNNTVAL 484
RB 431 MLATSPFVETKTFEEVCAKALLLNSGAFSGTGIMPLHNSAAGVSMIDPTTAL 490
QY 385 VWTAKSGISGQGSMLNLLMLSLGVHASKKMEHLINKCKNVVYVTLLEMLNA 444
RB 491 IYVLSGVLAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPVAPV 550
QY 445 HVL-----RCKS-----SITGSCFAPADSKSKSPG 474
RB 551 HVLHVPKAGSLGVHPPPSGSGAGGATAPASISASKRIESP 595

RESULT 32
ESRL_HORSE
ID ESRL_HORSE STANDARD: PRT: 594 AA
AC Q9TV98:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estradiol receptor (ER) (Estradiol receptor) (ER-alpha).
DS ER OR NR3A1 OR ESP.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
X 111
RF SEQUENCE FROM N.A.
RA McJownell K.J., Adams M.H., Green M.L., Cleaver B.D., Sharp D.C.;
RL Submitted (Jan 1999) to the EMBL/GenBank/DBJ databases.
CS 1-1 FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CS THE REGULATION OF ENDOCRINE GENE EXPRESSION AND AFFECT CELLULAR
CS PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES
CS 1-1 SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER
CS BETA (BY SIMILARITY).
CS 1-1 SUBCELLULAR LOCATION: Nuclear.
CS 1-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CS A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

DR	SMART: SM00440; H001: 1.	
DR	SMART: SM00399; ZNF_C4: 1.	
DR	PROSITE: PS00341; NUCLEAR_RECEPTOR: 1.	
KM	Proceptor; Transcription regulator; DNA-binding; Nuclear protein;	
KM	Zinc-finger; Steroid binding.	
FM	PFAM: 1	144
ET	SMART: 1	145
ET	SMART: 1	210
		REGULATING (BY SIMILARITY), NUCLEAR RECEPTOR TYPE.

FT ZN_FING 145 165 C4-TYPE.
 FT ZN_FING 181 205 C4-TYPE.
 FT ZN_FING 211 272 HINGE.
 FT ZN_FING 273 581 STEROID-BINDING (BY SIMILARITY)
 FT ZN_FING 261 265 POLY-GLY.
 FT ZN_FING 278 291 POLY-LEU.
 FT ZN_FING 469 474 POLY-LEU.
 FT ZN_FING 537 545 POLY-GLY.
 SC SOURCE: 581 AA; 63461 MW; D499B9E7B4B964 CIRC64.
 Query Match 47.0%; Score 1185.5; DB 1; Length 581;
 host local similarity 49.1%; Pred. No. 4e-90;
 Matches 264; Conservative 80; Mismatches 115; Indels 67; Gaps 14.
 3 YSTP-----SNVTNLEGGPGKQTSPNVLPPTGHSPLVYVHROLSHIVAPKSP 53
 43 YSAPLDHAGPDSGSLQSLGSP---TSPLVFVSSPLSLSPFM--HPSHHYLETSTIP 96
 54 WCFARSLHTLPVNRFLTKRK---VSGNRASPVTPGSGS-----KRDHPCAVGSDY 102
 97 -----VYRSSVPSQSSVSREDCOTSDSYSVSGGALAAQFLAKKRPVAVGSDY 151
 103 ASGVHYGVWSCTPFAKFPKSTQGHNDVLPATNGTTTKNRKSTYACTPKQYEVGMV 162
 152 ASGVHYGVWSCTPFAKFPKSTQGHNDVLPATNGTTTKNRKSTYACTPKQYEVGMV 211
 163 KQSFRRPGCYHIVRGRS-----ADEQLRAGKAKKSGGAPR 201
 212 KQSFRRPGCYHIVRGRS-----ADEQLRAGKAKKSGGAPR 264
 222 VRELLALSTQVLTLEAFPEVLSRF--SAFTEASMMMLINLANEIVHMSM 253
 270 I-----SNRPPOVILLLOGAPP MLCSKQKLNPTPEVIMMLTISMAKRELVHIMAM 322
 260 AKKIPGVLSLFTVAVRILFSWVWLVKMGIMWPSIDPBGKLEAFVILVPEDESKVEG 319
 323 AKKIPGVLSLFTVAVRILFSWVWLVKMGIMWPSIDPBGKLEAFVILVPEDESKVEG 382
 320 ILEIFMLATTSRPEFKLOHKEYLVKAMIIINSNYPVLTATQD-AUSSPKAHLIN 378
 383 MATIFMLATTSRPEFKLOHKEYLVKAMIIINSNYPVLTATQD-AUSSPKAHLIN 442
 379 AVTDAVWVIAKSGISSQSSQSNMLANLMLLSHVHASKGMEHLINRKNVIVYEL 438
 443 TTTDAVWVIAKSGISSQSSQSNMLANLMLLSHVHASKGMEHLINRKNVIVYEL 507
 439 IEMLNAM-VLRGCKSTTOSER--SPAEISKKEG 470
 503 IEMLNAM-VLRGCKSTTOSER--SPAEISKKEG 537
 RESULT 34
 ESR1_CREA
 ID ESR1_CREA STANDARD: PPT: 583 AA.
 AC P02407
 DI 01-OCT-1996 (Rel. 34, Created)
 DI 01-NOV-1997 (Rel. 35, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estrogen receptor (ER) (estradial receptor) (ER-alpha).
 GN ESR1 OR NR3A1 OR ESR.
 OS Oestrogenic androgen (estrogen) (estrogen).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 ON Nrr1_Pap1D-47669.
 RX SOURCE: FROM N.A.
 RX MEDLINE: 97120581; PubMed: 8961252;
 RA Tan N.S., Lam T.J., Ding J.L.;
 RI "transcription regulatory signals in the 5' and 3' regions of
 RI Oestrogenic androgen ER gene";
 RI Mol. Cell. Endocrinol. 123:149-161(1996).

RN [2]
 RP SOURCE: OF 270-583 FROM N.A.
 RC TISSUE: Blood;
 RX MEDLINE: 96272402; PubMed 877315;
 RA Tan N.S., Lam T.J., Ding J.L.;
 RI "Molecular cloning and sequencing of the hormone-binding domain of
 RI Oestrogenic androgen receptor gene";
 RL DNA Seq. 5:359-370(1995).
 CC FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC SUBMIT: BENDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 CC BETA (BY SIMILARITY).
 CC SUBCELLULAR LOCATION: Nucleat.
 CC DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.
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 CC or send an email to license@ebi.ac.uk).
 CC EMBL: X93557; CAA63774.1; JOINED.
 CC EMBL: X93558; CAA63774.1; JOINED.
 CC EMBL: X93559; CAA63774.1; JOINED.
 CC EMBL: X93560; CAA63774.1; JOINED.
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 CC EMBL: X93677; CAA63774.1; JOINED.
 CC EMBL: X93678; CAA63774.1; JOINED.
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 CC EMBL: X93680; CAA63774.1; JOINED.
 CC EMBL: X93681; CAA63774.1; JOINED.
 CC EMBL: X93682; CAA63774.1; JOINED.
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 CC EMBL: X93684; CAA63774.1; JOINED.
 CC EMBL: X93685; CAA63774.1; JOINED.
 CC EMBL: X93686; CAA63774.1; JOINED.
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 CC EMBL: X93689; CAA63774.1; JOINED.
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 CC EMBL: X93691; CAA63774.1; JOINED.
 CC EMBL: X93692; CAA63774.1; JOINED.
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D6	EMUL:	AE25:6005;	AA6:2454.1;	
D6	EMUL:	AE06:1275;	AA6:6548.1;	
D6	EMUL:	AE25:6006;	AA6:2454.1;	
D6	HSST:	PO8472;	LEPR:	
D6	InterPro:	IPR000536;	hormone_rec_1a	
D6	InterPro:	IPR001292;	oestrad_receptor	
D6	InterPro:	IPR001723;	steroid_receptor	
D6	InterPro:	IPR001628;	Znf_C4steroid	
D6	Pfam:	PF001045;	hormone_rec_1	
D6	Pfam:	PF02179;	oest_recpt_1	
D6	Pfam:	PF00398;	STEROHORM	
D6	PRINTS:	PR00047;	STEROHORMER	
D6	ProDom:	PD000475;	Znf_C4steroid_1	
D6	SMART:	SM00440;	RC011_1	
D6	SMART:	SM00593;	Znf_C4_1	
D6	PROSITE:	PS00041;	NUCLEAR_RECEPTOR_1	
KM	Receptor:	Transcription regulation	DNA binding; Nuclear protein;	
KW	Zinc finger	Steroid binding	Allosteric splicing	
FT	DOMAIN	1	386	
FT	DOMAIN	187	252	
FT	ZN_FING	187	207	
FT	ZN_FING	224	247	
FT	DOMAIN	254	315	
FT	DOMAIN	316	617	
FT	DOMAIN	321	325	
FT	DOMAIN	512	516	
FT	DOMAIN	577	591	
FT	VARIABLE	1	46	
FT	VARIABLE	1	425	
SD	SEQUENCE	617 AA;	67670 MW;	

best overall similarity 91.06; prec. NO. 96.67;
Matches 251; Conservative 73; Mismatches 110;
Indels 58; Gaps 14

49 -P\$NVTNLEGGPCROT\$P\$NVLWPTP\$H\$PLVH -KOLSHL.YALP

76. YSAVAPPEQIENI_QPTJPN: SS SPVVPVPSQI_SPTI(CHPPAQTQHTAQVQVYI.EPS 141

OKSOWITAKS LILLI L V N K H L J K K R V S S N K A S V I P C S K P O A I I P A V S 100

191201517KSSVLASAKSRVHLSABGRUDVIAVIASTPSGAHPSGALGLVKEIKRYCSVCS191

THE UNIVERSITY OF MICHIGAN LIBRARY

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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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248 SWANKI, POLYMER, AND FISH EMPLOYMENT AND FISHING VOLUME 217

464 AWAKKIVITHELO SHIMVOT EESSWELIMIGI EWS YIPSKI LEADOTIKSPOVV 474

418 POLITEKHMAL'NISHI I KHIMIKAT'SKIYE VESTI I NAUKI O SVETLE

4.2.4 H(CMAF:1)I(M,I,A)VAKF:K(T,I,K)S(F:H)V(LKA)I(I,NSC)A(F:S)C(SS)V(F:P)K(D)I(MVQ)M 483

477. INAVTIDALVWVIAKSI;ISSQUCSMRI,ANI,MI,LSIVRIASNK,MEHL,MMK;KNVIVYI) 446.

484 MDNITDAILYYISQSI SVQIQSRQAJ.L.L.L.SHI RIMSYKGMHLLY SMK'KNKVP.YI) 544

437 I.I.I.F.M.N.I.I.V.I.R 448

544 1.1.1. E.M.I. > A.H.K.I. R 555

RESULT	48
ESR1.CONCMY	STANDARD; PRG: 662 AA.
DT	ESR1.CONCMY
AC	P16058.GPHS79, GPHS78, UYGGE;
DT	01-APR-1990 (Ref. 14, treated)
DT	16-OCT-2001 (Ref. 40, last sequence update.)
DJ	15-JUN-2002 (Ref. 41, last annotation update)
DE	ESTROGEN RECEPTOR (ER) (Estrogen receptor) (ER-alpha).
CN	ENSR.NR3A1 OR ESR-
OS	Oncorhynchus mykiss (Rainbow trout) .
OC	Eukaryota; Metazoa; Chordata; Teleostei; Euteleostomi;
OC	Aet. teleostei; Neopterygii; Teleostei; Euteleostei;
OC	Prochordates; Teleostei; Salmoniformes; Salmonidae; Oncorhynchus.
OX	NB1 (taxid: 8022);
RN	[1]
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).
KX	MEDLINE: 91066824; PubMed 22100411.
KX	Parkkel P., Le Gall F., Je Gust P., Valotiaine Y.;
KT	"Full-length sequence and in vitro expression of rainbow trout
KT	estrogen receptor cDNA.";
RL	Mol. Cell. Endocrinol. 71:195-204(1990).
RN	[2]
RP	SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
KC	ILLUSTRATION;
KC	ILLUSTRATION;
KX	MEDLINE: 20114660; PubMed 10650938;
KA	Parkkel P., Melivior R., Flontot G., Valotiaine Y.;
KT	"Two estrogen receptor (ER) isoforms with different estrogen
KT	dependencies are generated from the trout Er gene.";
RL	Endocrinology 141:571-580(2000).
RN	[3]
RP	SEQUENCE OF 150-574 FROM N.A. (SHORT ISOFORM).
KT	ILLUSTRATION;
KX	MEDLINE: 89127284; PubMed 29156448;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 16, 2003, 11:34:03 ; Search time 27.487 seconds

(without alignments)
3575.671 Million cell updates/sec

Title: US-08-826-361a-5

Percent score: 25.22
Sequence: 1 MMSVSPSNVTNLEKSPKQOT PPSVAFKSKSPKSPNLSQ 477

Scoring table: BIOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum hit seq length: 0
Maximum hit seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 120 comparisons

Database:

1: SPITRMBL_21:
2: SP_archaea:
3: SP_bacteria:
4: SP_fungi:
5: SP_human:
6: SP_invertebrate:
7: SP_mammal:
8: SP_mhc:
9: SP_oranella:
10: SP_plant:
11: SP_rodent:
12: SP_virus:
13: SP_vertebrate:
14: SP_unclassified:
15: SP_virus:
16: SP_bacteria:
17: SP_archaea:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	2241	88.5	593	11	Q91286	Q91286 mus musculus
2	2141	84.9	499	6	Q95M60	Q95M60 macaca aethi
3	2058	81.6	486	6	Q95M69	Q95M69 gallus gallus
4	1558.5	61.8	542	13	Q90W56	Q90W56 squilla
5	1369	54.3	553	13	Q90W58	Q90W58 brachydanio
6	1360	53.9	553	13	Q90W57	Q90W57 brachydanio
7	1354	53.7	552	13	Q90W59	Q90W59 brachydanio
8	1354	53.7	552	13	Q90W59	Q90W59 brachydanio
9	1295.5	51.4	562	13	Q90W75	Q90W75 brachydanio
10	1243	49.3	250	6	Q95JCO	Q95JCO canis familiaris
11	1211	48.0	587	13	Q90W40	Q90W40 canis familiaris
12	1210	48.0	581	13	Q90W49	Q90W49 canis familiaris
13	1181.5	46.8	569	13	Q90W59	Q90W59 brachydanio
14	1170.5	46.4	554	13	Q90W51	Q90W51 brachydanio
15	1165.5	46.2	431	6	Q95L13	Q95L13 canis familiaris
16	1156	45.8	578	13	Q90W40	Q90W40 canis familiaris

17	1141.5	45.3	620	13	Q90W56	Q90W56 brachydanio
18	1113	44.1	554	13	Q90W58	Q90W58 brachydanio
19	1099	43.6	458	13	Q90W53	Q90W53 brachydanio
20	1061.5	42.1	391	13	Q90W58	Q90W58 brachydanio
21	942.5	37.4	335	13	Q90W54	Q90W54 brachydanio
22	679	25.9	274	13	Q91984	Q91984 brachydanio
23	594.5	23.6	200	13	Q90W59	Q90W59 brachydanio
24	525	20.8	101	11	Q923V1	Q923V1 mesocricetus
25	522	20.7	484	5	Q90W59	Q90W59 brachydanio
26	522	20.7	495	5	Q90W59	Q90W59 brachydanio
27	517.5	20.5	159	6	Q95JCO	Q95JCO canis familiaris
28	504	20.1	249	6	Q95JCO	Q95JCO canis familiaris
29	504	20.0	710	13	Q91H05	Q91H05 canis familiaris
30	479	19.0	593	13	Q90W54	Q90W54 brachydanio
31	475.5	18.9	323	13	Q90W54	Q90W54 brachydanio
32	470.5	18.7	703	13	Q90W54	Q90W54 brachydanio
33	461	18.3	438	13	Q90W57	Q90W57 brachydanio
34	460.5	18.3	689	13	Q90W55	Q90W55 brachydanio
35	459.5	18.2	742	13	Q90W59	Q90W59 brachydanio
36	458.5	18.2	525	6	Q95L13	Q95L13 canis familiaris
37	458	18.2	934	6	Q95L13	Q95L13 canis familiaris
38	452.5	17.9	414	11	Q90W50	Q90W50 mus musculus
39	449.5	17.8	400	5	Q91448	Q91448 amblyomma americanum
40	448.5	17.8	436	5	Q915C6	Q915C6 biotaphia
41	448.5	17.8	688	13	Q90W58	Q90W58 brachydanio
42	448	17.8	790	13	Q90W48	Q90W48 xenopus laevis
43	442	17.5	87	6	Q90W52	Q90W52 sus scrofa
44	442	17.5	157	13	Q90W52	Q90W52 sus scrofa
45	442	17.5	848	13	Q90W59	Q90W59 brachydanio
46	441.5	17.5	401	13	Q90W56	Q90W56 brachydanio
47	440.5	17.5	360	13	Q92274	Q92274 crocodilus
48	437	17.3	982	6	Q90W58	Q90W58 brachydanio
49	436	17.3	414	5	Q91449	Q91449 amblyomma americanum
50	435	17.2	363	5	Q90W51	Q90W51 polyandria
51	434	17.2	906	4	Q90W51	Q90W51 polyandria
52	433	17.2	82	6	Q90W58	Q90W58 brachydanio
53	432	17.1	412	13	Q91840	Q91840 xenopus laevis
54	432	17.1	730	4	Q13771	Q13771 homo sapiens
55	431.5	17.1	793	11	Q90W50	Q90W50 mus musculus
56	431.5	17.1	794	11	Q90W50	Q90W50 mus musculus
57	430.5	17.1	895	6	Q90W59	Q90W59 brachydanio
58	430.5	17.1	896	6	Q90W59	Q90W59 brachydanio
59	430	17.0	853	13	Q91245	Q91245 onchocerca
60	429.5	17.0	427	5	Q90W58	Q90W58 brachydanio
61	427.5	17.0	692	13	Q90W54	Q90W54 brachydanio
62	426	16.9	763	13	Q90W57	Q90W57 brachydanio
63	425	16.9	340	5	Q90W58	Q90W58 brachydanio
64	425	16.9	854	13	Q91244	Q91244 onchocerca
65	423.5	16.8	344	4	Q90W51	Q90W51 polyandria
66	423	16.8	438	13	Q90W58	Q90W58 brachydanio
67	421.5	16.7	769	13	Q90W59	Q90W59 brachydanio
68	421	16.7	849	13	Q90W52	Q90W52 sus scrofa
69	419	16.6	379	13	Q90W51	Q90W51 polyandria
70	417	16.5	452	13	Q91613	Q91613 xenopus laevis
71	417	16.5	563	13	Q90W54	Q90W54 brachydanio
72	416.5	16.5	346	4	Q14267	Q14267 homo sapiens
73	416.5	16.5	475	5	Q90W51	Q90W51 polyandria
74	415.5	16.5	448	5	Q90W53	Q90W53 brachydanio
75	414.5	16.4	427	13	Q90W56	Q90W56 brachydanio
76	411.5	16.3	303	6	Q90W54	Q90W54 brachydanio
77	411	16.3	422	13	Q90W51	Q90W51 polyandria
78	409	16.2	389	5	Q90W59	Q90W59 brachydanio
79	408	16.2	380	5	Q90W54	Q90W54 brachydanio
80	405	16.1	797	13	Q90W55	Q90W55 brachydanio
81	404.5	16.0	344	13	Q91445	Q91445 amblyomma americanum
82	403	16.0	438	5	Q90W51	Q90W51 polyandria
83	403	16.0	763	13	Q90W57	Q90W57 brachydanio
84	399	15.8	322	11	Q90W51	Q90W51 polyandria
85	396	15.7	539	11	Q90W50	Q90W50 mus musculus
86	396	15.7	540	11	Q90W50	Q90W50 mus musculus
87	392	15.5	407	13	Q90W53	Q90W53 brachydanio
88	387.5	15.4	467	5	Q90W51	Q90W51 polyandria
89	385	15.3	541	4	Q90W50	Q90W50 mus musculus

DB 147 DQHL LNRENIKKKKIAPV--GSSVNVVSKRDHIFAVNDPASCYHGVMSYEDKAFK 194
 QY 121 KSGTGRNVYGVAVN--TIDNKKRSYVAGTLEKCYVWYKSGRPFEPYKRVVHGGV 190
 DB 194 KRSYGRNAYGVAVN--TIDNKKRSYVAGTLEKCYVWYKSGRPFEPYKRVVHGGV 254
 QY 181 SAQDQALQACAKARSG GRAPVRRRLDIALSPQGVTLTLEAPPIV--TSRPAFPE 238
 DB 254 LSSAOQJMSKCKRSGISDTFRLISQCLNHLAERKLSSLEAFEPNVSLNHKKPYTE 314
 QY 249 ASMMSTFKALKEIVYMISMAKRTGVETSLFQVRLLESTWMEVIMMIMMSIDHF 298
 DB 414 VSMMSFTNLADRELVIIMAMARKVGFVEVLDHGVVLEECMEVIMVGLMMSYEP 374
 QY 299 GKLFAPVLDIDRECKVSEGLETFDMLATTSRPRELKQREYVYKAMILLNSMY 358
 DB 474 GKLFAPVLDIDRECKVSEGLETFDMLATTSRPRELKQREYVYKAMILLNSMY 444
 QY 459 PLVATQDALSSKRLAHNLAVTDALVWYIASKGISGQGSRIANLMLSHVHNSNR 418
 DB 444 ERSQVTEHNRKREKRLH--TIDNKKRSYVAGTLEKCYVWYKSGRPFEPYKRVVHGGV 494
 QY 419 ERSQVTEHNRKREKRLH--TIDNKKRSYVAGTLEKCYVWYKSGRPFEPYKRVVHGGV 464
 DB 494 GMEIDVYMKRKVNVVYDILMLAHV--KSSITSSGSPATD 544

RESULT 5

DB QYRSM7 PRELIMINARY: PRT: 554 AA.
 AC QYRSM7:
 DT 01-JUN-2001 (TEMBR-rel. 19, created)
 DT 01-JUN-2001 (TEMBR-rel. 19, last sequence update)
 DT 01-JUN-2002 (TEMBR-rel. 21, last annotation update)
 DE ZEPER beta42 protein.
 DN ZEPER BETA2.
 OS Brachydonto retio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 OX NCBI_TaxID 7955;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Menzel A., Pollock J.E., Andrade L., Blaise O., Landel V., Koh O.,
 Kockel F.:
 KT "Binding characteristics, transactivation properties and central
 BL expression of three estrogen receptor subtypes in zebrafish."
 CC 1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC 2. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DE EMBL: A014567; C059449.1;
 DB InterPro: IPR000546; hormone_rec_119;
 DB InterPro: IPR001628; ZnF_C4steroid.
 DB Pfam: PF00104; hormone_rec_1.
 DB PRINTS: PR00105; Z1-C4_1.
 DB PRODOM: PD00045; ZnF_C4steroid_1.
 DB PRODOM: PD00045; ZnF_C4steroid_1.
 DB SMART: SM00499; ZNF_C4_1.
 DB SMART: SM00499; ZNF_C4_1.
 DB PROSITE: PS00041; NUCLEAR RECEPTOR; DNKNMNL.
 KW DNA binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc finger.
 SN SEQUENCE: 554 AA; 8450DEG7AC0F5ED C0664;

Query Match 54.88; Score 1469; DB 14; Length 554;
 Post Local Similarity 58.28; Prod. No. 60-118;
 Matches 270; Conservative 65; Mismatches 108; Indels 20; Gaps 7;
 QY 18 KQTSRNVNVPVTSLSPLVNIHQSLVAFQKSNWFAFSP EPTLVNRPETLKKYSG 77
 DB 83 KQTSRNVNVPVTSLSPLVNIHQSLVAFQKSNWFAFSP EPTLVNRPETLKKYSG 142
 QY 78 NRCASVTVDSKRDHIFAVNDPASCYHGVMSYEDKAFKRSIGSHNYGVAVN 147
 DB 144 TEETS--VSLKRAKMHVAVNDPASCYHGVMSYEDKAFKRSIGSHNYGVAVN 200

QY 148 CTIDNKKRSYVAGTLEKCYVWYKSGRPFEPYKRVVHGGV--TIDNKKARSKS 195
 DT 201 CTIDNKKRSYVAGTLEKCYVWYKSGRPFEPYKRVVHGGV--TIDNKKARSKS 256
 QY 196 QYHAPVYV--PTITDIALSPQGVTLTLEAPPIV--TSRPAFPAFAMMSL 245
 DB 257 GPRSQELKSTPRDLSQNVVRLISPEELSRMEAFPEYVLMKMKPFPAFAMMSL 316
 QY 246 LALAEVYIMTSMARKTGVETSLFQVRLLESTWMEVIMMIMMSYEPYKRVVHGGV 305
 DB 317 TNLADKRLVIMTSMARKTGVETSLFQVRLLESTWMEVIMMIMMSYEPYKRVVHGGV 376
 QY 306 DVLVDRCKVSEGLETFDMLATTSRPRELKQREYVYKAMILLNSMY YELVAT 364
 DB 377 DLSLPSQSCVQGLVEITFDMLATTSRPRELKQREYVYKAMILLNSMY TASSSG 416
 QY 465 QDALSSKRLAHNLAVTDALVWYIASKGISGQGSRIANLMLSHVHNSNRKMEHL 424
 DB 447 EDQSRKSLCLDSVTDALVWYIASKGISGQGSRIANLMLSHVHNSNRKMEHL 496
 QY 425 NMKRVNVVYDILMLAHV--KSSITSSGSPATD ERSK 467
 DB 497 GMMKRVNVVYDILMLAHV--KSSITSSGSPATD ERSK 540

RESULT 6

DB QYRSM7 PRELIMINARY: PRT: 554 AA.
 AC QYRSM7:
 DT 01-JUN-2001 (TEMBR-rel. 17, created)
 DT 01-JUN-2001 (TEMBR-rel. 17, last sequence update)
 DT 01-JUN-2002 (TEMBR-rel. 21, last annotation update)
 DE Estrogen receptor beta4.
 OS Brachydonto retio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 OX NCBI_TaxID 7955;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Akten B., Kishida M., Gullard G.V.:
 KT "Estrogen receptor gamma in zebrafish."
 BL Submitted (FEB-2001) to the EMBL/GenBank/DDB databases.
 CC 1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DE EMBL: AF49414; AKR15742.1;
 DB HSSP: P03372; IERR.
 DB InterPro: IPR000546; hormone_rec_119;
 DB InterPro: IPR001724; Steroid_receptor.
 DB InterPro: IPR001628; ZnF_C4steroid.
 DB Pfam: PF00104; hormone_rec_1.
 DB PRINTS: PR00498; STEROIDHORMONER.
 DB PRINTS: PR00498; STEROIDHORMONER.
 DB PRODOM: PD00047; STEROIDHORMONER.
 DB PRODOM: PD00047; STEROIDHORMONER.
 DB SMART: SM00499; ZNF_C4_1.
 DB SMART: SM00499; ZNF_C4_1.
 DB PROSITE: PS00041; NUCLEAR RECEPTOR; DNKNMNL.
 KW DNA binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc finger.
 SN SEQUENCE: 554 AA; 62210 MW; A30DC08H01DHFID C0664;

Query Match 54.98; Score 1360; DB 14; Length 554;
 Post Local Similarity 57.88; Prod. No. 4-10-117;
 Matches 268; Conservative 66; Mismatches 110; Indels 20; Gaps 7;
 QY 18 KQTSRNVNVPVTSLSPLVNIHQSLVAFQKSNWFAFSP EPTLVNRPETLKKYSG 77
 DB 83 KQTSRNVNVPVTSLSPLVNIHQSLVAFQKSNWFAFSP EPTLVNRPETLKKYSG 142
 QY 78 NRCASVTVDSKRDHIFAVNDPASCYHGVMSYEDKAFKRSIGSHNYGVAVN 147
 DB 144 TEETS--VSLKRAKMHVAVNDPASCYHGVMSYEDKAFKRSIGSHNYGVAVN 200


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Db 143 THEETS--VSLRGKAIHMYGAVCSFYASGVHCVMSDEGCKAPFKKSTGCHNDYTGPAING 200
OY 148 CTIDKRRPSQAMPIKCYEVGMKCGSPREPOYLVPKPSAMDP--LHCACAKRS 195
Db 201 CTIDKRRPSQAMPIKCYEVGMKCGSPREPOYLVPKPSAMDP--LHCACAKRS 256
OY 196 GCHAPPVR-----ELLDALSPKQVLTLLAEPRHV-LISRPASPTFASMMNL 245
Db 257 GPRSPKSLIPRLSNFVPLSLSPKLSPLMEAPPELYLMKMKPTEAAVMMSL 416
OY 246 IRLAKETVHMSWAKIPFVELSLFVNPVLPESQMEVLMKIMWSPREKELFAP 305
Db 317 FNADKELVHMSWAKIPFVELSLFVNPVLPESQMEVLMKIMWSPREKELFAP 376
OY 306 DLVLDRECKVYGLLEIFDMLLATTSPREKLOKREYLVKAMILLNSM-YPLVAT 464
Db 377 DLCTSPRESCVGLVFPVPMILATSPREKLOKREYLVKAMILLNSM-LGSSRG 436
OY 365 GMDISSKRLAHILNAVTDALVWVIAKSGISSQOSKRLANILMLSHVPHASNGKMHLL 424
Db 437 EDILOSRSKILCVLIDSTDAVMAISTKTSQSPKSTRIAHILMLSHVPHASNGKMHLL 496
OY 425 NMKCKVNVVYDILFPMNAHVLPGKSSITSPSPSA-EDSKS 467
Db 497 GMRKCKVNVYDILFPMNAHVLPGKSSITSPSPSA-EDSKS 549
RESULT 7
OY08K9 PRELIMINARY: PRT: 565 AA.
AC OY08K9:
DT 01-JUN-2002 (TEMBLrel. 21, created)
DT 01-JUN-2002 (TEMBLrel. 21, last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, last annotation update)
DE Estrogen receptor beta.
GN ERB.
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Notolestei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Pleuronectiformes;
OC Pleuronectiformes; Paratichthyidae; Paratichthys.
OX NCBI_taxonomy:8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Sakimura N., Takamune K., Nagahama Y., Abe S.;
RT "Role of estrogen receptor in gonadal sex differentiation in Japanese
RT flounder (Paratichthys olivaceus).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AH070630; BAB85623.1;
KW Receptor.
SQ SEQUENCE 565 AA: 62521 MW: 742488.14248070 CIRC64.
Query Match 53.7%; Score 1361; DB 13; Length 565;
Best Local Similarity 56.7%; Pred. No. 1,5e-116;
Matches 276; Conservative 60; Mismatches 130; Indels 22; Gaps 10.
OY 2 NYSIFSNVLEGGNG-KOTTSPNVLPFPCHLS-PLVHR-QLSHVAEPKSPWPAF 58
Db 72 SYAPSS---LPCFVHOSLSPLFWPSHIMPMIHSQNSGQNPQPSWMT 127
OY 59 SLHLLPVRKELKRVSNRPAAPVTPDSSKRAHFAVSTAAVRYVWSTP 118
Db 128 PRGVLA-ANSKVPVR SQFSEGVVSSKRSGLHYCAVCHVAVSVWVWVWV 164
OY 119 FPRSTGGNVYTPVTPNCTITKREKSGVAFKPEYGVNVRNSKPEFQYR-AY 176
Db 185 FFKRSISGGNDYTPVTPNCTITKREKSGVAFKPEYGVNVRNSKPEFQYR-AY 241
OY 177 PPGSALFETPWACAFKPGVAPFVETLTAISPTVLTATFTHV 177
Db 245 PRTTRISSGPAKPAITGPVVALMNPLOPAPITFPIIPINAFPVIVIAMTWSGP 404
OY 246 FTASMMMLIKLAKELVHMSWAKIPFVELSLFVNPVLPESQMEVLMKIMWSP 296

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Db 405 LLEAVNMSLTRIALDELVMTWAKIPFVELSLFVNPVLPESQMEVLMKIMWSP 464
OY 296 DHEKLEFAVGLVDEKCKVEGLEIFPMILATSPREKLOKREYLVKAMILLNS 455
Db 465 DHEKLEFAVGLVDEKCKVEGLEIFPMILATSPREKLOKREYLVKAMILLNS 424
OY 456 SM-YPLVATQDASSKRLAHILNAVTDALVWVIAKSGISSQOSKRLANILMLSHVPH 414
Db 425 NMCTSSGSEFELHSKILLIDVAVTDALVWVIAKSGISSQOSKRLANILMLSHVPH 484
OY 415 ASKRGMHILNMKCKVNVVYDILFPMNAHVLPGKSSITSPSPSA-EDSKS 466
Db 485 VSNRGMDHCKMKMVVLYDILFPMNAHVLPGKSSITSPSPSA-EDSKS 544
OY 467 SKRASON 473
Db 545 SONSSN 551
RESULT 8
OY08S9 PRELIMINARY: PRT: 592 AA.
AC OY08S9:
DT 01-DEC-2001 (TEMBLrel. 19, created)
DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, last annotation update)
DE ZHR beta1 protein.
GN ZPER-BETA1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_taxonomy:7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Meunier A., Pellegrini E., Anglade I., Haise O., Landet V., Kah O.;
RA Pakdel F.;
RT "Binding characteristics, transactivation properties and central
RT expression of three estrogen receptor subtypes in zebrafish.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL: AJ14566; GAC93848.1;
DR InterPro: IPR000345; Cyt_c_heme_bind.
DR InterPro: IPR000546; Hormone_rec_119.
DR InterPro: IPR001628; Zn1_C4steroid.
DR Pfam: Pf00104; hormone_rec_1.
DR Pfam: Pf00105; zf-C4_1.
DR ProDom: FDC00035; Zn1_C4steroid_1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKN:UN.1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; UNKN:UN.1.
KW DNA binding, Nuclear protein, Receptor, Transcription regulation,
KW Zinc finger.
SQ SEQUENCE 592 AA: 66046 MW: 76521862034188 CIRC64.
Query Match 53.7%; Score 1364; DB 13; Length 592;
Best Local Similarity 56.7%; Pred. No. 1,6e-116;
Matches 281; Conservative 63; Mismatches 98; Indels 54; Gaps 12.
OY 27 SAWEWLPVR---SQVVRQSHVYATPWSVTAWSVTAWSVTAWSVTAWSV 72
Db 72 SPILLNV-PSHMDPPEKALVSKH-----SWEAKI--LLSSSSLSITKILG 141
OY 73 EKNSGAGVGLGKRAHFAVSNVASYGVWVSCHDYATFKRSQCHNDYTG 142
Db 142 GCHAPPVR-----ELLDALSPKQVLTLLAEPRHV-LISRPASPTFASMMNL 201
OY 143 THEETS--VSLRGKAIHMYGAVCSFYASGVHCVMSDEGCKAPFKKSTGCHNDYTGPAING 200
Db 201 CTIDKRRPSQAMPIKCYEVGMKCGSPREPOYLVPKPSAMDP--LHCACAKRS 256
OY 196 GCHAPPVR-----ELLDALSPKQVLTLLAEPRHV-LISRPASPTFASMMNL 245
Db 257 GPRSPKSLIPRLSNFVPLSLSPKLSPLMEAPPELYLMKMKPTEAAVMMSL 416
OY 246 IRLAKETVHMSWAKIPFVELSLFVNPVLPESQMEVLMKIMWSPREKELFAP 305
Db 317 FNADKELVHMSWAKIPFVELSLFVNPVLPESQMEVLMKIMWSPREKELFAP 376
OY 306 DLVLDRECKVYGLLEIFDMLLATTSPREKLOKREYLVKAMILLNSM-YPLVAT 464
Db 377 DLCTSPRESCVGLVFPVPMILATSPREKLOKREYLVKAMILLNSM-LGSSRG 436
OY 365 GMDISSKRLAHILNAVTDALVWVIAKSGISSQOSKRLANILMLSHVPHASNGKMHLL 424
Db 437 EDILOSRSKILCVLIDSTDAVMAISTKTSQSPKSTRIAHILMLSHVPHASNGKMHLL 496
OY 425 NMKCKVNVVYDILFPMNAHVLPGKSSITSPSPSA-EDSKS 467
Db 497 GMRKCKVNVYDILFPMNAHVLPGKSSITSPSPSA-EDSKS 549

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Db	PVNHETLEKREVSSESTASPIJTSSEKPIAHFVANSVAVSHVWMS*EODKAFKREKSI	60
QY	125 QGINDYGTATNCTTIDKPKRSGCZACPIKRYEVGWKQSSPREFGUYPIVENDGKADE	144
Db	61 QGINDYGTATNCTTIDKPKRSGCZACPIKRYEVGWKQSSPREFGUYVWPKQSSDE	120
QY	185 QLEHACAKKRSQGHATREVELLDIALSPGQVLTLLLEAPRHVLTSPRSAGFTASMMSS	244
Db	121 QLEHLSKAKKNQGHATREVELLDIALSPGQVLTLLLEAPRHVLTSPRSSTPFTASMMSS	160
QY	245 LTPIANPVIYHMI*SMARKIPGCVFESLFDQVLELSE*MMEVLMKGLMMS*LDHKGKILFA	304
Db	181 LTKLADKELVHMI*GMARKIPGCVFESLFDQVLELSE*MMEVLMKGLMMS*IGHKGKILFA	240
QY	305 PDEVLIDHDS 314	
Db	241 PDEVLIDHDS 250	

	RESULT 11	
GRUWBO	PREDMAINMARY:	PR1: 587 AA.
AC	GRUWBO:	
D1	01-MAR-2002 (TFMBRL-1_20, Created)	
D1	01-MAR-2002 (TFMTRL-1_29, last sequence update)	
D1	01-JUN-2002 (TFMTRL-1_21, last annotation update)	
DE	Estrogen receptor.	
CN	ER.	
OS	Caiman crocodilus (Speckled caiman) (Caiman sclerops).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Crocodylidae; Alligatorinae; Caimana.	
OX	NCHI_TaxID=8499;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
FX	MEDLINE:21490797; PubMed:11601222;	
KA	Sumida K., Ise N., Saito K., Kaneko H.;	
RT	"Molecular cloning and characterization of reptilian estrogen receptor cDNAs."	
RI	Mol. Cell. Endocrinol. 183:33-39(2001).	
DL	EML: AB055220; BAB79436.1;	
DR	InterPro: IPRO00536; Hormone_Fam_119	
DR	InterPro: IPRO01297; Estrogen_Receptor	
DR	InterPro: IPRO01723; Steroid_Receptor	
DR	InterPro: IPRO01628; ZnF_C4Steroid	
DR	Pfam: PF00104; hormone_rec.1	
DR	Pfam: PF02159; oest_recep.1	
DR	Pfam: PF00105; z1-C4_1	
DR	PRINTS: PR00398; STROHOMONR	
DR	PRINTS: PR00047; STROIDEINCR	
DR	ProDom: PD000035; ZnF_C4steroid_1	
DR	SMART: SM00430; HOL1_1	
DR	SMART: SM00499; ZNF_C4_1	
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1	
KW	Receptor.	
SQ	SEQUENCE 587 AA; 66514 MW; D617E2B837FF613 CRC64;	
QUERY MATCH	48.08; Score 1211; DB 13; Length 587;	
Best Local Similarity	55.08; Prod. No. 2.6e+103;	
Matches 2461	Conserved: 71; Missed: 106; Indels: 24; Gaps: 8	
DY	22 SPVAVTMTDTHGVTVVHFCISHTATPEKSLGCFASLEHLITLVSELTIPVSTGM 78	
DB	100 SPVAVTMTDTHGVTVVHFCISHTATPEKSLGCFASLEHLITLVSELTIPVSTGM 156	
DY	79 PAAAPTPDPY : SRPDAIPVAAGSYAAYHWASCPFKAPFTSTGMACTG 15	
DB	157 PPAASSTSEKASI SMESTKETFPYAVGNVASVHYVWSFGCKATFAETLGTHNIMEL 216	
DY	134 ATHQCTDKRRKRSGCATFERFYVNAVVGSSPPPGYGLVLYPLGSATFEIAGATGA 19	
DB	217 ATHQCTDKRRKRSGCATFERFYVNAVVGSSPPPGYGLVLYPLGSATFEIAGATGA 276	
DY	194 RSGGHAFPV--PELLLD AISPVLITLFAPPPIVLS--PSAPTEAW 241	

DB	277	TAEMPTLEMTSPVJIKHTEKNSPAISIAEOMFALLPEPVPYSEYDOPPEFPMAS	346
QY	242	MSLSIEJALPELVIMHSMARKIDGVELSTPQVQVELSTPWEVVEL29M0LIMPSJODHCKI	301
DB	337	MTLLTILADBELVIMHNMKRVKPGVDLTJLHQVILJLZAMLELIMJQVWKSMBHCKI	306
QY	402	LEAPDVLIDPEBZVVEJLELTHMLAISTPEKJQKBLJCVWAMLLNSMRYPL	461
DB	497	LEFANILLDNDQKVEWNAVELEPMLATAAFPEPMNJCDEEPTVKSTILINSVYTEL	456
QY	462	IAQVADUSPEKPAHLLNAVPAIWMVAFKSSISQWSEMLATIMLEHVAHANSYM	420
DB	457	SSTLEKSEPEQVJHEVLEKTPYTLIHMKSSELQOQBRLAOLLLSHIPEHMSCKM	516
QY	421	PHILLNKSKRVVYDYLEEMNAVIL	447
DB	517	PHILNKKSKRVVYDYLEEMDAHIL	543

ID	ORGANISM	PRELIMINARY	PKT	581 AA
AC	080WAV			
01	01-MAR-2002 (Tremature)	20, Created		
02	01-MAR-2002 (Tremature)	20, Last sequence update		
03	01-JUN-2002 (Tremature)	21, Last annotation update		
04	Estrogen receptor			
05	Chimaphorus umbellatus (Whitetail lily)			
06	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
07	Lepidodactylus; Squamata; Scleroglossa; Scleromorphia; Tetrapoda;			
08	Tetrapoda; Chimaphorus			
09	NCBI_TaxID=37197;			
10	Sequence from N.A.			
11	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
12	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
13	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
14	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
15	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
16	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
17	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
18	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
19	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
20	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
21	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
22	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
23	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
24	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
25	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
26	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
27	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
28	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
29	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
30	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
31	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
32	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
33	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
34	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
35	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
36	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
37	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
38	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
39	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
40	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
41	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
42	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
43	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
44	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
45	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
46	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
47	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
48	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
49	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
50	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
51	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
52	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
53	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
54	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
55	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
56	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
57	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
58	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
59	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
60	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
61	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
62	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
63	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
64	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
65	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
66	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
67	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
68	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
69	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
70	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
71	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
72	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
73	Accession: U00001.1; Length: 581; Type: Coding sequence (CDS)			
74	Accession: U00001.1;			

284 EVIMMELMRSIDHCKLIFAVDLVDHCECKVCHLEIFEMILATISPEPELKIORRE 344
 470 ELLIVHWPSTIPPEGLHFAVNIICOPDANVPMILKPEMLLVSPPEPELORRE 426
 444 YLCVKAMLLNSM-VPIVATATODSSKLAHLINAVTDAIWWIAKSGSSQOOSRI 402
 430 VYIAKAMLLNSGVEFCISAGROTNVQLIQDILEKMDAGSTTHTASNPQHSRI 486
 403 ANIMLISHVRIASNKMEHLNKKCNVIVYDILLMLNHLKGRSSITGSESP 461
 490 SOLLELSOIRHISNKGIEHLSMKRKVPIPEYDLELLEDAHSION-----TGLRSP 544

RESULT 19

Q990J3 PRELIMINARY: PRI: 458 AA.

AC Q990J3
 DT 01-MAR-2001 (TEMBREL: 16, Created)
 DT 01-MAR-2001 (TEMBREL: 16, Last sequence update)
 DT 01-JUN-2002 (TEMBREL: 21, Last annotation update)
 DE Estrogen receptor (Fragment).
 GN ER.
 OS Homo sapiens.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Perciformes; Perciformes;
 OC Actinopterygii; Neopterygii; Teleostei; Perciformes; Perciformes;
 OC Labridae; Halichoeres.
 OX NCBI_TaxID:147432;
 RN 111
 RP SEQUENCE FROM N.A.
 KA Kim S.J., Koi G., Takemura A., Nakamura M.
 RT Partial sequence and expression of estrogen and estrogen receptor
 RT genes in the protozoans, wassie, halichoeres trimaculatus.
 RL Submitted (08-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC EMBL: AF346401; AAC4841.1;
 DR HSSP: P03372; IERR.
 DR InterPro: IPR000546; Hormone_rec_119.
 DR InterPro: IPR001723; Steroid_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam: PF00104; hormone_rec_1.
 DR Pfam: PF00105; zf-C4_1.
 DR PRINTS: PR00398; STRHORMNER.
 DR PRINTS: PR00047; STRHORMNER.
 DR ProDom: PD000035; Znf_C4steroid_1.
 DR SMART: SM00430; HOL1_1.
 DR SMART: SM00499; Znf_C4_1.
 DR PROSITE: PS00041; NUCLEAR_RECEPTOR_1.
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc finger.
 FT NON_TER 1 1
 ST SEQUENCE 458 AA: 51319 MW: 019482332119777 CPE64:

Query Match 43.6%; Score 1099; DB 13; Length 458;
 best local similarity 56.2%; Prod. No. 4.46 93;
 Matches 240; Conservative 64; Mismatches 85; Indels 40; Gaps 10;

QY 91 PIAHPVAVSYVASSTHYVWVSPTKAPF+PSIGSHNDYTPDANQOTLKRPKSVQA 150
 DB 23 KEMRYAVSYVASSTHYVWVSPTKAPF+PSIGSHNDYTPDANQOTLKRPKSVQA 82
 QY 151 GPVRYVAVSYVASSTHYVWVSPTKAPF+PSIGSHNDYTPDANQOTLKRPKSVQA 197
 DB 83 CHIRFYVAVSYVASSTHYVWVSPTKAPF+PSIGSHNDYTPDANQOTLKRPKSVQA 146
 QY 198 HARVPFIIIDAS--PQVVIITIFAPFHWISPP--SAVEFASMMMSIPLADEL 254
 DB 137 NATIVEENPQWISMPDQVLLDQVATP--IIVSRKISPEYEVIMLITLSMADREL 195
 QY 254 VHIISAKKIPGVEISLEQVPILESQMEVLMGIMIPRSIDHCKLIFAVDLVDHCE 413

DB 196 VHIISAKKIPGVEISLEQVPILESQMEVLMGIMIPRSIDHCKLIFAVDLVDHCE 255
 QY 414 QKCVENIIEFMILATISPEPELKIORREYIVAKMILNNSMYPIVATQD ALESSPK 472
 DB 256 QKCVENIIEFMILATISPEPELKIORREYIVAKMILNNSMYPIVATQD ALESSPK 416
 QY 473 LAHLINAVTDAIWWIAKSGSSQOOSRIANIMLISHVRIASNKMEHLNKKCNVIV 432
 DB 416 VQMDITITDAIHHISQSAHQSPPQVITITISHPMKSKMEPHYSMKRPKNV 476
 QY 433 PYVILLEMIMNAHVL----GGRKS-SITGSESPASHSKRSQSONQS 476
 DB 476 PYVILLEMIMNAHVL----GGRKS-SITGSESPASHSKRSQSONQS 424

RESULT 20

Q98SM8 PRELIMINARY: PRI: 391 AA.

AC Q98SM8
 DT 01-JUN-2001 (TEMBREL: 17, Created)
 DT 01-JUN-2001 (TEMBREL: 17, Last sequence update)
 DT 01-JUN-2002 (TEMBREL: 21, Last annotation update)
 DE Estrogen receptor gamma (Fragment).
 GN Brachydanio rerio (zebrafish) (Zebra danio).
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID:7955;
 RN 111
 RP SEQUENCE FROM N.A.
 KA Aktien B., Kishida M., Gullard G.V.
 RT "Estrogen receptor gamma in zebrafish."
 RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC EMBL: AF349413; AAK16741.1;
 DR HSSP: P03372; IHCO.
 DR InterPro: IPR000546; Hormone_rec_119.
 DR InterPro: IPR001723; Steroid_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam: PF00104; hormone_rec_1.
 DR Pfam: PF00105; zf-C4_1.
 DR PRINTS: PR00398; STRHORMNER.
 DR PRINTS: PR00035; Znf_C4steroid_1.
 DR SMART: SM00430; HOL1_1.
 DR SMART: SM00499; Znf_C4_1.
 DR PROSITE: PS00041; NUCLEAR_RECEPTOR_1.
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc finger.
 FT NON_TER 1 1
 ST SEQUENCE 391 AA: 44663 MW: 458681666816591 CPE64:

Query Match 42.1%; Score 1061.5; DB 13; Length 391;
 best local similarity 58.2%; Prod. No. 1e-89;
 Matches 219; Conservative 55; Mismatches 67; Indels 45; Gaps 7;

QY 133 PAINQSTIEKPKPKVAVRIKCYEVVWVSCPPPVVYVVKQK-----SAVEQL 186
 DB 1 PATNQSTIDKSPKPKVAVRIKCYEVVWVSCPPPVVYVVKQK-----SAVEQL 60
 QY 187 HCAKAKR-----SGHAPVRELLDASPEQVITLLEAPPHVILSKP 242
 DB 61 GLEPGSQOHFPIPSQSHPIPSQSHV-EGPEL-----NVSPEQVITLLEAPPHVILSKP 116
 QY 233 -SAPFPAASMMSTKLAKELVHMSYAKKIPGVEISLEQVPILESQMEVLMGIMIP 291
 DB 117 VKRPVTFASMMSTKLAKELVHMSYAKKIPGVEISLEQVPILESQMEVLMGIMIP 176
 QY 292 WPSIDHCKLIFAVDLVDHCECKVCHLEIFEMILATISPEPELKIORREYIVAKM 351
 DB 177 WPSIDHCKLIFAVDLVDHCECKVCHLEIFEMILATISPEPELKIORREYIVAKM 246
 QY 452 LLNSMYPIVAT--QPAISSKRIADILNAVIAIWWIAKSGSSQOOSRIANIMLIS 410


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DB 237 LINSNMSSSLPGLPEVSEKCVLMILSVYDALVWILSKIGLSSQDSIFLALMLLS 296
|||||
UY 411 HVHANSKCEHLLMKKKNVYVVDLLEMLNAILVGRK-----SSTSSGSP 461
|||||
DB 297 HHHNSKCEHLLSNKKRNVALYDLEMLDNTSSSRMLEDRDSDPENLHFSHDP 456
|||||
UY 462 AELSKSESSONSOS 477
|||||
DB 457 LKKSIOGELPHSKAE 472
|||||

RESULT 21
Q90024 PRELIMINARY: PRT: 435 AA.
AC Q90024:
DE 01-MAR-2001 (TREMURel: 16, created)
DE 01-MAR-2001 (TREMURel: 16, last sequence update)
DE 01-JUN-2002 (TREMURel: 21, last annotation update)
DE Estrogen receptor subtype 1 (Fragment).
OS Micropterus salmoides (largemouth bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Perciformes; Percoidae;
OC Centrarchidae; Micropterus
OX NCBI_TaxID 2706;
RN [1]
RP SEQUENCE FROM N.A.
RA Bowman C.J., Sabo Attwood T., Dowling N.B.,
RA "Estrogen with bass Estrogen receptor subtype 1 partial cDNA sequence."
RA Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
KT Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
FT 1: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CV 1: SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DE EMBL: AF254062; AAC44622.1;
DE HSSP: P03472; IBCV.
DE InterPro: IPR000536; Hormone_rec_119.
DE InterPro: IPR01728; Steroid_receptor.
DE InterPro: IPR01628; Zn_finger_cisrod.
DE Pfam: PF00104; hormone_rec_1.
DE Pfam: PF00105; ZF_C4_1.
DE PRIN1: PR00398; STROHOMNER.
DE PRIN1: PR00047; STROHDEFINER.
DE Tracem: PR000035; Zn_finger_cisrod_1.
DE SMART: SM00430; ZnF1_1.
DE SMART: SM00398; Znf_C4_1.
KM DNA binding. Nuclear protein. Receptor. Transcription regulation.
KW Zinc finger.
FT NON-TER 435 435
PT SEQUENCE 435 AA: 47768 MW: 40594650.004976 CYS64;
SU QUERY MATCH
Host Local Similarity 47.48; Score 942.5; DB 13; Length 435;
Matches 193; Conservative 51; Mismatches 69; Indels 89; Gaps 72

DB 104 SYHYGVSGCEKKAFFKSTQENNYGYPATNGCTLKKKRSYVRLKRYEVANV 193
|||||
UY 2 SISHYGVSGCEKKAFFKSTQENNYGYPATNGCTLKKKRSYVRLKRYEVANV 193
|||||
DB 164 GYSRRRCYRIVRKRSK-----DQGLAVKAKRSKHAVVR 203
|||||
UY 62 GYVRKRR GRVLRKRRKRRCTMDRKSKDLFYTPVDPDKRSSSVAQRRKRS 117
|||||
DB 204 HLLDALSPQVLTLLFAFPVVLISD--SAPPTASMMSTLTK-----LADNL 253
|||||
UY 118 --VGMSPDQVLTLLGAEPVAV--MISRKLSRPTEVTMLLTSMARKELVMADEL 173
|||||
DB 254 VHMISWARKLPQVLSLTQVRLJESQWMEVLMGIMKRSIDHGRKLFAFDVLGRDE 413
|||||
DB 174 VHMISWARKLPQVLSLTQVRLJESQWMEVLMGIMKRSIDHGRKLFAFDVLGRDE 233
|||||
UY 414 GKVVECTLEFPMILATSPPEPKIGRKYVAVAMILLNSMWYAVTAYGD AASSPV 472
|||||

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DB 234 GKVVECTLEFPMILATSPPEPKIKPPEVCTKALLLNSAFSPVCTIMETLNSVE 293
|||||
UY 473 LAHLINAVTALVWYIAKSGISSQDSMRILANLMLSHVRI 414
|||||
DB 294 VHMISWARKLPQVLSLTQVRLJESQWMEVLMGIMKRSIDHGRKLFAFDVLGRDE 435
|||||

RESULT 22
Q91984 PRELIMINARY: PRT: 276 AA.
AC Q91984:
DE 01-OCT-2000 (TREMURel: 15, created)
DE 01-OCT-2000 (TREMURel: 15, last sequence update)
DE 01-MAR-2002 (TREMURel: 20, last annotation update)
DE Estrogen receptor alpha (Fragment).
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID 7955;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE LIVER.
RA Leight J., Broekhof J.L.M., Brouwer A., Lanier P.H., Mink A.J.,
RA Van der Stad E.T., Verhaak D.A., Wester F., Zivkovic D.,
RA Van der Burg B.J.
RA "A novel in vivo bioassay for (xeno)estrogens using transgenic
RA zebrafish."
KT Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DE EMBL: AF275910; CAB77022.1;
DE HSSP: P03472; IBCV.
DE InterPro: IPR000536; Hormone_rec_119.
DE InterPro: IPR01728; Steroid_receptor.
DE Pfam: PF00104; hormone_rec_1.
DE PRIN1: PR00398; STROHOMNER.
DE SMART: SM00430; ZnF1_1.
KM Receptor.
FT NON-TER 276 276
PT SEQUENCE 276 AA: 40926 MW: 201247854.294665 CYS64;
SU QUERY MATCH
Host Local Similarity 26.98; Score 679; DB 13; Length 276;
Matches 147; Conservative 47; Mismatches 61; Indels 28; Gaps 62

DB 159 VGVNRCGRRECGYRLVRKRC-----SADQLHRAQ-----KAKRSRIA 199
|||||
DB 1 VGVNRCGRRECGYRLVRKRC-----SADQLHRAQ-----KAKRSRIA 199
|||||
UY 200 PVRELLDALSPQVLTLLFAFPVVLISD--SAPPTASMMSTLTKADRTVMTS 258
|||||
DB 60 STL-----GMSPDQVLTLLGAEPVAV--SRKLSRPTEVTMLLTSMARKELVMA 113
|||||
UY 259 WARKLPQVLSLTQVRLJESQWMEVLMGIMKRSIDHGRKLFAFDVLGRDE 418
|||||
DB 114 WARKLPQVLSLTQVRLJESQWMEVLMGIMKRSIDHGRKLFAFDVLGRDE 173
|||||
UY 419 GILEFPMILATSPPEPKIGRKYVAVAMILLNSMWYAVTAYGD AASSPV 477
|||||
DB 174 GMAETPMILATSPPEPKIGRKYVAVAMILLNSMWYAVTAYGD AASSPV 233
|||||
UY 478 NAVTALVWYIAKSGISSQDSMRILANLMLSHVRIASNMGM 420
|||||
DB 234 DNLIALVYISKRSASQDSMRILANLMLSHVRIASNMGM 276
|||||

RESULT 23
Q90259 PRELIMINARY: PRT: 200 AA.
AC Q90259:
DE 01-DEC-2001 (TREMURel: 19, created)
DE 01-DEC-2001 (TREMURel: 19, last sequence update)
DE 01-MAR-2002 (TREMURel: 20, last annotation update)

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[illegible]

[illegible]

KM	Receptor:	
SC	SEQUENCE:	689 AA; 76.416 MW; F0610B5AC7A72A6 C1R054;

DNA-binding: Nuclear protein; Receptor; Transcription regulation; SMART: SM00499; UniProt: 1, PROSITE: PS00041; NUCLEAR_RECEPTOR: 1.

prostate; P500041; NUCLEAR_RECEPTOR; 1; DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger

GENOTYPE	PRELIMINARY:	PRELIMINARY:
01 MAR 2002 (TREMUR)	20, (Treated)	
02 01 MAR 2002 (TREMUR)	20, (Last sequence update)	
03 01 JUN 2002 (TREMUR)	21, (Last annotation update)	
04 Similar to tremurid X receptor beta.		
05 Mus musculus (Mouse).		
06 Eukaryotic Metazoa: Chordata; Crustacea; Vertebrata; Euteleostomi;		
07 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
08 Mus Taxid 100903;		
09 11		
10 SPECIMEN FROM N.A.		
11 TISSUE: LIVER;		
12 ST. LOUIS, MO, U.S.A.		
13 Submitted (Feb. 2001) to the EMBL/GenBank/TrEMBL databases.		
14 EMBL: AF019452; AM19452.1;		
15 GenBank: AF000536; Hormone_rec_1.fq.		
16 InfoProc: PR000172; StChrm_receptor.		
17 InfoProc: PR000628; Znf_C4.fq.		
18 Pfam: PF00104; hormone_rec_1.		
19 Pfam: PF00105; z1_c4_1.		
20 PRINTS: PR00098; STROHOMNR.		
21 PRINTS: PR00047; STROIDFMR.		
22 ProDom: PD000045; Znf_C4StroId_1.		
23 SMART: SM00430; H011_1.		
24 SMART: SM00399; Znf_C4_1.		
25 PROSITE: PS00041; NOCTEAL_RECEPTOR; UNKNOWN_1.		
26 Record		
27 SOURCE: 414 AA; 44839 MB; 6241974145-677069 CDS; 64;		

[illegible]


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Db      84 GIKASIKHYGVSYSTKGGFFKRTVKKLSYVPPPTITIKRQBNQYGVYQK----140
QY      160 GNVKGGSPRRPGVAVRPPSADQIHWCKAKSGSHAPVRLIIPALSPQVETL 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      141 --LAKMKRFAVDERRTKDADSEV-----RSTSGAP-----PRMLERI 181
QY      220 LEAPPHVIISPPSAPTFASM----MMSITKIAKELVHMSAKKIPGHVLSIEVY 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182 LEAE---LRVESQTIILSESAGQDPVSSIQQAIDRLQILOWAKHPIHEEILEDK 238
QY      276 PLEFVWVEMLMIMWESTIPPKITAPPVVITPPGKVFELIFEMLIA-TISPF 324
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      239 VLLKAWNFIITAASSHPSVVPQSVIATPIVVPRIHAGCA-GVGAIFPVLLVAKM 297
QY      335 PEIKIQHRYGVKAMILLNSMPVITATVANSPELA----HLLNAVIVAVVIAK 390
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      298 REMKMURFELGLAVVLEPFACKLRTYSNGEGSVSALEFHCRQYDP-----349
QY      391 SGLSSQGSMBLNLMLISHVHASNKGMHELLNMKKNVVPYDILLMLNA 444
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      350 -----QPGFAKILLRLPALRSGLKTEHLPFKLIDTPIDNFLSMLEA 496

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RESULT 40

QRTSC6

ID QRTSC6; PRELIMINARY; PRI: 436 AA.

DI 01-JUN-2002 (JREML001, 21, Created)

DI 01-JUN-2002 (JREML001, 21, Last sequence update)

DI 01-JUN-2002 (JREML001, 21, Last annotation update)

DE RKR-like protein.

GN RKR.

OS Biomphalaria glabrata (bloodfluke planorb).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basmatiaophora;

OC Planorbidae; Biomphalaria.

OX NCBI_taxid=6526;

RN [1]

RP SEQUENCE FROM N.A.

RA Brown M., Mendoza P.L., Noel C., Escriba H., Cornette J., Landet V.,

RT "A conserved RKR family nuclear receptor from the mollusc Biomphalaria

glabrata.";

RI Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.

RL EMBL: AY048663; AAL86461.1; -

SV SEQUENCE 436 AA; 4825 MW; 94D6P84BSGHRH4F9 CRC64;

Query Match 17.8%; Score 448.5; DB 5; Length 436;

Host Local Similarity 30.1%; Pred. No. 5,8e-33;

Matches 132; Conservative 63; Mismatches 170; Indels 79; Gaps 14;

```

QY      15 GRRPQTSNNVLPTRHSPVVAHQIASHIYAPRYKSPWCEAPSLHRTLVNPEITLKK 71
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      55 GRRGMSSASSTOPSPG---POGMHSPGMHSTSSMGSP-----PM-----92
QY      75 VSGNRCASPVTPSP-----GSKRAHFGAVSDVASYHYGVWSYFGYKAFKPSIQ 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      93 ----LGLSP-SRPSRPLRHSSITHKICAIQGVASGKHGVVSCDQKGFERRIVK 147
QY      127 HNIYTPALNCTIIRKNEKSYVACPIKGYVAVWVCGSPREPGYPLVPPGSAVDQI 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      148 DITVAIKRKNMIMQKPDGNPQYVTKMKPSMKPFAVQEF-----QVFFPGDSEV 202
QY      187 WVAGVAPSGSHAPPELIPALSPEDVLTLEAFPHVLLSKVATFTIANMRRSL 215
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      203 E---STSGANNIMVDEQLLEALAVIRKIDITYITADQKV-----TNI 242
QY      246 TKIAKELVHMSAKKIPGEVELSLPDVRLISQWMEVLMGLMRSIDHPKLIAP 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      243 GQADAKQIFETVWAKRIPHEITELPEVYVILLACWNELLTACSHSTMAKIDILLAT 302
QY      306 PIVLDPPGKGVGLIEFDMLA--TISPEELKIQHRYGVKAMILLNSMPVITATV 364
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      303 GIVHPSAH-QAGVETIDPVLTIVAKMIMKMLTELGLVAVVLEPFACGL-TAV 360

```

```

QY      465 QHAISSPKLAHLINAVIATVWVIAKSGTSSQWQSMPIANIMLSHPPA-NKGMHLL 424
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      361 QEVQILREKVY-----ASLEEVTKS--RYPEHGRFAKILLKIPALRSIGLKLEHCP 411
QY      425 NMKKNVVPYDILLML 442
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      412 FFKLIDQDPTDIFLMBML 429

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Search completed: June 15, 2003, 14:15:09
 Job time : 32.487 secs

GenScore version 5.1.6
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us-08-826-361a-6

Run on: June 16, 2003, 04:20:57 : Search time 109.628 seconds
(without alignments)
505,642 Million pairs of alignments

File: US-08-826-361a-6

Portlet score:

Sequence: 1 MNSYSPNTNIEFGPGPOT QGSMELANMISVPEAP 416

Scoring table:

BLASTM62

Scorched: 908470 seqs, 13350620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database:

1: A_Genoseq_101002.*
2: /S1US2/4/qdata/4/genoseq/genoseq-emb1/AA1980.FAI.*
3: /S1US2/4/qdata/4/genoseq/genoseq-emb1/AA1981.FAI.*
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12: /S1US2/4/qdata/4/genoseq/genoseq-emb1/AA1990.FAI.*
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23: /S1US2/4/qdata/4/genoseq/genoseq-emb1/AA2001.FAI.*
24: /S1US2/4/qdata/4/genoseq/genoseq-emb1/AA2002.FAI.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being filtered, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	FR	TD	Description
1	2203	100.0	416	18	AAW43213
2	2203	100.0	416	23	AAW47837
3	2203	100.0	416	18	AAW43214
4	2203	100.0	416	23	AAW47836
5	2198	99.8	477	18	AAW43212
6	2198	99.8	477	23	AAW47834
7	2198	99.8	477	18	AAW47835
8	2198	99.8	477	23	AAW43215
9	2198	99.8	477	18	AAW47838
10	2198	99.8	477	23	AAW43217

11	2198	99.8	540	22	AAW27422	Human oestrogen re
12	2198	99.8	540	22	AAW60649	Human oestrogen re
13	2198	99.8	540	23	AAW47835	Full length estro
14	2198	99.8	548	20	AAW07270	Human oestrogen re
15	2198	99.8	793	23	AAW80756	Amino acid sequen
16	2179	98.9	485	20	AAW01597	Human oestrogen re
17	1985	90.1	549	20	AAW94125	Mouse oestrogen re
18	1983	90.0	549	20	AAW04434	Mouse oestrogen re
19	1981	89.9	445	18	AAW14723	Human oestrogen re
20	1981	89.9	445	18	AAW14723	Human oestrogen re
21	1972.5	89.5	445	21	AAW51946	Human oestrogen re
22	1966	89.2	450	20	AAW04433	Human oestrogen re
23	1965	89.2	455	18	AAW14725	Human oestrogen re
24	1964	89.2	567	20	AAW98128	Mouse oestrogen re
25	1728.5	78.5	510	20	AAW04435	Mouse oestrogen re
26	1728.5	78.5	510	20	AAW98126	Mouse oestrogen re
27	1499	68.0	414	20	AAW98127	Human oestrogen re
28	1499	68.0	740	20	AAW04436	Human oestrogen re
29	1375.5	48.8	542	22	AAW38227	Human oestrogen re
30	1065	48.3	547	23	AAW81600	Human oestrogen re
31	1065	48.3	595	22	AAW84509	Human oestrogen re
32	1065	48.3	595	22	AAW84512	Human oestrogen re
33	1064	48.3	581	23	AAW83791	Human oestrogen re
34	1063	48.3	595	20	AAW21626	Human oestrogen re
35	1063	48.3	595	22	AAW84505	Human oestrogen re
36	1063	48.3	595	22	AAW84506	Human oestrogen re
37	1063	48.3	595	22	AAW84513	Human oestrogen re
38	1063	48.3	595	23	AAW67478	Human oestrogen re
39	1060	48.1	595	22	AAW84507	Human oestrogen re
40	1056.5	48.0	575	23	AAW19430	Human oestrogen re
41	1056	47.9	595	22	AAW84508	Human oestrogen re
42	1056	47.9	595	22	AAW84514	Human oestrogen re
43	1054	47.8	595	22	AAW84510	Human oestrogen re
44	1054	47.8	595	22	AAW84511	Human oestrogen re
45	1054	47.8	595	22	AAW84512	Human oestrogen re
46	1054	47.8	595	23	AAW84513	Human oestrogen re
47	1054	47.8	595	23	AAW84514	Human oestrogen re
48	1054	47.8	595	23	AAW84515	Human oestrogen re
49	1054	47.8	595	23	AAW84516	Human oestrogen re
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51	1054	47.8	595	23	AAW84518	Human oestrogen re
52	1054	47.8	595	23	AAW84519	Human oestrogen re
53	1054	47.8	595	23	AAW84520	Human oestrogen re
54	1054	47.8	595	23	AAW84521	Human oestrogen re
55	1054	47.8	595	23	AAW84522	Human oestrogen re
56	1054	47.8	595	23	AAW84523	Human oestrogen re
57	1054	47.8	595	23	AAW84524	Human oestrogen re
58	1054	47.8	595	23	AAW84525	Human oestrogen re
59	1054	47.8	595	23	AAW84526	Human oestrogen re
60	1054	47.8	595	23	AAW84527	Human oestrogen re
61	1054	47.8	595	23	AAW84528	Human oestrogen re
62	1054	47.8	595	23	AAW84529	Human oestrogen re
63	1054	47.8	595	23	AAW84530	Human oestrogen re
64	1054	47.8	595	23	AAW84531	Human oestrogen re
65	1054	47.8	595	23	AAW84532	Human oestrogen re
66	1054	47.8	595	23	AAW84533	Human oestrogen re
67	1054	47.8	595	23	AAW84534	Human oestrogen re
68	1054	47.8	595	23	AAW84535	Human oestrogen re
69	1054	47.8	595	23	AAW84536	Human oestrogen re
70	1054	47.8	595	23	AAW84537	Human oestrogen re
71	1054	47.8	595	23	AAW84538	Human oestrogen re
72	1054	47.8	595	23	AAW84539	Human oestrogen re
73	1054	47.8	595	23	AAW84540	Human oestrogen re
74	1054	47.8	595	23	AAW84541	Human oestrogen re
75	1054	47.8	595	23	AAW84542	Human oestrogen re
76	1054	47.8	595	23	AAW84543	Human oestrogen re
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79	1054	47.8	595	23	AAW84546	Human oestrogen re
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82	1054	47.8	595	23	AAW84549	Human oestrogen re
83	1054	47.8	595	23	AAW84550	Human oestrogen re
84	1054	47.8	595	23	AAW84551	Human oestrogen re
85	1054	47.8	595	23	AAW84552	Human oestrogen re
86	1054	47.8	595	23	AAW84553	Human oestrogen re
87	1054	47.8	595	23	AAW84554	Human oestrogen re
88	1054	47.8	595	23	AAW84555	Human oestrogen re
89	1054	47.8	595	23	AAW84556	Human oestrogen re
90	1054	47.8	595	23	AAW84557	Human oestrogen re
91	1054	47.8	595	23	AAW84558	Human oestrogen re
92	1054	47.8	595	23	AAW84559	Human oestrogen re
93	1054	47.8	595	23	AAW84560	Human oestrogen re
94	1054	47.8	595	23	AAW84561	Human oestrogen re
95	1054	47.8	595	23	AAW84562	Human oestrogen re
96	1054	47.8	595	23	AAW84563	Human oestrogen re
97	1054	47.8	595	23	AAW84564	Human oestrogen re
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101	1054	47.8	595	23	AAW84568	Human oestrogen re
102	1054	47.8	595	23	AAW84569	Human oestrogen re
103	1054	47.8	595	23	AAW84570	Human oestrogen re
104	1054	47.8	595	23	AAW84571	Human oestrogen re
105	1054	47.8	595	23	AAW84572	Human oestrogen re
106	1054	47.8	595	23	AAW84573	Human oestrogen re
107	1054	47.8	595	23	AAW84574	Human oestrogen re
108	1054	47.8	595	23	AAW84575	Human oestrogen re
109	1054	47.8	595	23	AAW84576	Human oestrogen re
110	1054	47.8	595	23	AAW84577	Human oestrogen re
111	1054	47.8	595	23	AAW84578	Human oestrogen re
112	1054	47.8	595	23	AAW84579	Human oestrogen re
113	1054	47.8	595	23	AAW84580	Human oestrogen re
114	1054	47.8	595	23	AAW84581	Human oestrogen re
115	1054	47.8	595	23	AAW84582	Human oestrogen re
116	1054	47.8	595	23	AAW84583	Human oestrogen re
117	1054	47.8	595	23	AAW84584	Human oestrogen re
118	1054	47.8	595	23	AAW84585	Human oestrogen re
119	1054	47.8	595	23	AAW84586	Human oestrogen re
120	1054	47.8	595	23	AAW84587	Human oestrogen re

84	5733.5	26.0	458	20	AAV038337	Human EGR4
85	5733.5	26.0	458	21	AAV039655	Human EGR4
86	5733.5	26.0	458	21	AAV83823	Human EGR4
87	5722.5	26.0	418	21	AAV83824	Human EGR4
88	5722.5	26.0	433	9	AAV80931	Sequence of human
89	5722.5	26.0	433	21	AAV039666	Human EGR4
90	5722.5	26.0	433	21	AAV82970	Human EGR4
91	5722.5	26.0	500	20	AAV03836	Human EGR4
92	5722.5	26.0	500	21	AAV83822	Human EGR4
93	5722.5	26.0	508	20	AAV204657	Human EGR4
94	5703.5	25.9	418	20	AAV03838	Human EGR4
95	5643.5	24.6	486	23	AAV03347	Human EGR4
96	5643.5	24.6	552	22	AAV80411	Human EGR4
97	5640.5	24.5	521	9	AAV80300	Sequence of human
98	5293.5	24.0	556	22	AAV841197	Human EGR4
99	5122.5	23.2	484	22	AAV84251	Human EGR4
100	5004.5	22.9	99	22	AAV37173	Human EGR4
101	4448.5	20.3	933	20	AAV210621	Human EGR4
102	4448.5	20.3	933	21	AAV97297	Human EGR4
103	4440.5	20.0	918	12	AAV812243	Human EGR4
104	4339.5	19.9	839	23	AAV686238	Human EGR4
105	4337.5	19.8	452	29	AAV210627	Human EGR4
106	4337.5	19.8	918	20	AAV334391	Human EGR4
107	4337.5	19.8	919	10	AAV931099	Human EGR4
108	4337.5	19.8	919	10	AAV909966	Human EGR4
109	4337.5	19.8	919	18	AAV814783	Human EGR4
110	4337.5	19.8	919	21	AAV78914	Human EGR4
111	4337.5	19.8	919	23	AAV19061	Human EGR4
112	4337.5	19.7	144	20	AAV384236	Human EGR4
113	4334.5	19.7	144	20	AAV084227	Human EGR4
114	4334.5	19.7	144	20	AAV084227	Human EGR4
115	4312.5	19.6	984	9	AAV80923	Sequence of the hu
116	4311.5	19.6	984	20	AAV216222	Human EGR4
117	4311.5	19.6	902	12	AAV812224	Human EGR4
118	4288.5	19.4	902	10	AAV93110	Human EGR4
119	4288.5	19.4	902	10	AAV93110	Human EGR4
120	4288.5	19.4	777	9	AAV809139	Sequence of the hu

A1.1 (NM:NTS)

RES01ET 1	
AAW44214	
ID	AAW44214 standard; Protein: 416 AA.
XX	
Ac	AAW44214;
XX	
DE	20 APR 1998 (first entry)
XX	
DE	Human oestrogen receptor protein exon B splice variant.
XX	
XX	Oestrogen receptor protein; steroid; alternative splicing; estradiol;
XX	estrogen; estradiol; screening.
XX	
OS	Homo Sapiens.
XX	
EN	EF798478 A2.
XX	
XX	01 OCT 1997.
XX	
FE	25 MAR 1997; 97EP 020903.
XX	
XX	
FE	22 NOV 1996; 96EP 020484.
XX	
XX	26 MAR 1996; 96EP-0209820.
XX	
FA	(AIKU) AK27; N00EL NV.
XX	
FE	01 Jkema R; Moss-Iman St;
XX	
DE	W01; 1997 474188/44.
XX	
XX	N FSHB; AATB6443.
XX	

[illegible]

XX 25-MAR-1997: 2001EP-0200201.
 XX 26-MAR-1996: 96EP-0200820.
 XX 22-NV-1996: 96EP-0204284.
 XX 25-MAR-1997: 97EP-0200903.
 XX (AIKU) AKZO NOBEL NV.
 XX Mosselman S. Dijkema R.
 XX WP1: 2002-084444/12.
 XX N-PSDB: AAI72151.
 XX New isolated chimeric receptor comprising a DNA binding domain and/or
 XX liquid binding domain of a new estrogen receptor. For identifying
 XX functional ligands or hormonal analogs for the receptor.
 XX Example H: Page 17-18; 45pp; English.

XX The sequences given in AAB47836 and AAB47837 show splice variants
 XX of a novel estrogen receptor (ER). The gene encoding this new ER is
 XX located on chromosome 14 and has a different tissue distribution from
 XX classical ER. This ER also has two orphan ER's, ER-alpha and ER-beta.
 XX These orphan receptors have estrogen receptor related structure but do
 XX not appear to be able to bind estradiol or other ER ligands. These
 XX splice variants differ from the parent ER around exon 8. One clone
 XX contains exon 8b through alternative splicing. This causes an immediate
 XX termination of the reading thereby creating a truncation of the carboxy
 XX terminus. The other splice variant contains an alternative exon 8c, exon
 XX 8c, which encodes two C-terminal amino acids and has a stop codon.
 XX The splice variant proteins do not contain the AF-2 region and therefore
 XX probably lack the ability to modulate transcription of target genes in
 XX a ligand dependant manner. However they may be able to interact with
 XX the functioning of the WT classical ER or the novel ER of the invention,
 XX either by heterodimerisation or by occupying estrogen response elements
 XX or by interactions with other transcription factors.

XX Sequence 416 AA:

Query Match: 100.0%; Score 2203; DB 23; Length 416;
 Best Local Similarity 100.0%; Pred. No. 6; 3e-202;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 MNSYISNVNLEGGGROTTSPNVIWPHGLSPVYVHROLSHLYAEPOKSPWCEAKSL 60
 DB 1 MNSYISNVNLEGGGROTTSPNVIWPHGLSPVYVHROLSHLYAEPOKSPWCEAKSL 60
 YY 61 EHTLPVNRKELKRVSGNPGASVPTGNSKPAHPVAVSGDYASVYHGVMSGPGVAF 120
 DB 61 EHTLPVNRKELKRVSGNPGASVPTGNSKPAHPVAVSGDYASVYHGVMSGPGVAF 120
 YY 121 KRSLEGGNHYTPATNGCTTDRNPKRSYVACPLKRYVGVGMVSGSPREPGYPLVPGQR 180
 DB 121 KRSLEGGNHYTPATNGCTTDRNPKRSYVACPLKRYVGVGMVSGSPREPGYPLVPGQR 180
 YY 181 SAEOLHCAKAKRSKSHAPVPELIMASPEQVITLFAFPHAVISPSAPETAS 240
 DB 181 SAEOLHCAKAKRSKSHAPVPELIMASPEQVITLFAFPHAVISPSAPETAS 240
 YY 241 MMSSTKLAKKEIVHMSAKKIPGVELSTDQVILKSPVMEVIMMIMWSIFHHCK 300
 DB 241 MMSSTKLAKKEIVHMSAKKIPGVELSTDQVILKSPVMEVIMMIMWSIFHHCK 300
 YY 301 LIFAPPIVLDPKRGKVPETLFTFPMIAFTSPPEPKFGHEFYGVAMIIISNMYG 360
 DB 301 LIFAPPIVLDPKRGKVPETLFTFPMIAFTSPPEPKFGHEFYGVAMIIISNMYG 360
 YY 361 VTAIOLADSSRKLAHLINAVDALVAVTAKSCISQAGSMPILANIMISHPVAP 416
 DB 361 VTAIOLADSSRKLAHLINAVDALVAVTAKSCISQAGSMPILANIMISHPVAP 416

RESULT 4
 AAB478214
 ID AAB478214 standard: protein; 418 AA.
 XX
 AC AAB478214;
 XX
 DI 20-APR-1998 (first entry)
 XX
 DE Human oestrogen receptor protein splice variant (exon 8c).
 XX
 KW oestrogen receptor protein; steroid; alternative splicing; estradiol;
 XX
 KM estrone; estril; screening.
 XX
 OS Homo sapiens.
 XX
 PN EP798378-A2.
 XX
 PD 01-OCT-1997.
 XX
 XX 25-MAR-1997: 97EP-0200903.
 XX
 XX 22-NV-1996: 96EP-0204284.
 XX
 XX 26-MAR-1996: 96EP-0200820.
 XX
 XX (AIKU) AKZO NOBEL NV.
 XX
 XX Dijkema R. Mosselman S.
 XX
 XX WP1: 1997-473188/44.
 XX
 XX N-PSDB: AAI88414.
 XX
 XX DNA encoding estrogen receptor - useful in screening assay to
 XX identify novel ligands or hormonal analogues
 XX
 XX Claim 4: Page 30-32; 45pp; English.

XX This sequence represents a splice variant of a novel estrogen binding
 XX protein isolated from human thymus tissue. This protein contains an
 XX alternative exon 8 (exon 8c) of the novel estrogen receptor represented
 XX in AAB88412. This novel receptor is able to bind and be activated by
 XX estradiol, estrone and estril, can be used in a screening assay for the
 XX identification of new drugs e.g. novel ligands or hormonal analogues.
 XX This variant does not contain an AF-2 region and therefore probably
 XX lacks the ability to modulate transcription of target genes in a ligand
 XX dependent fashion.

XX Sequence 418 AA:

Query Match: 100.0%; Score 2203; DB 18; Length 418;
 Best Local Similarity 100.0%; Pred. No. 6; 3e-202;
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 1 MNSYISNVNLEGGGROTTSPNVIWPHGLSPVYVHROLSHLYAEPOKSPWCEAKSL 60
 DB 1 MNSYISNVNLEGGGROTTSPNVIWPHGLSPVYVHROLSHLYAEPOKSPWCEAKSL 60
 YY 61 EHTLPVNRKELKRVSGNPGASVPTGNSKPAHPVAVSGDYASVYHGVMSGPGVAF 120
 DB 61 EHTLPVNRKELKRVSGNPGASVPTGNSKPAHPVAVSGDYASVYHGVMSGPGVAF 120
 YY 121 KRSLEGGNHYTPATNGCTTDRNPKRSYVACPLKRYVGVGMVSGSPREPGYPLVPGQR 180
 DB 121 KRSLEGGNHYTPATNGCTTDRNPKRSYVACPLKRYVGVGMVSGSPREPGYPLVPGQR 180
 YY 181 SAEOLHCAKAKRSKSHAPVPELIMASPEQVITLFAFPHAVISPSAPETAS 240
 DB 181 SAEOLHCAKAKRSKSHAPVPELIMASPEQVITLFAFPHAVISPSAPETAS 240
 YY 241 MMSSTKLAKKEIVHMSAKKIPGVELSTDQVILKSPVMEVIMMIMWSIFHHCK 300
 DB 241 MMSSTKLAKKEIVHMSAKKIPGVELSTDQVILKSPVMEVIMMIMWSIFHHCK 300
 YY 301 LIFAPPIVLDPKRGKVPETLFTFPMIAFTSPPEPKFGHEFYGVAMIIISNMYG 360
 DB 301 LIFAPPIVLDPKRGKVPETLFTFPMIAFTSPPEPKFGHEFYGVAMIIISNMYG 360


```

|||||
1b 11FAPPLVLDROEGKVEGILEFDMALISPEHELMGHEFVYKAMILLNSMYPL 600
yy 661 VVATVADLSKRKAHLNNAVITATVAVTAKSSISGQOSMRANLMLLSVVRK 416
1b 661 VVATVADLSKRKAHLNNAVITATVAVTAKSSISGQOSMRANLMLLSVVRK 416

RESULT 4
AA047846 standard: protein: 418 AA.
xx AA047846:
xx
xx 25 MAR 2002 (first entry)
xx
xx ER splice variant ER alpha.
xx
xx DNA binding domain; LBD; ligand binding domain; LBD; chimera receptor;
xx estrogen receptor; ER; chromosome 14; ER-alpha; ER-beta; exon 8; 5'UTR;
xx estradiol; nuclear receptor; progesterone receptor; amplity; primer;
xx polymerase chain reaction; AF-2 region; splice variant.
xx
xx Homo sapiens.
xx
xx ER1162264 A2.
xx
xx 12 DEC 2001.
xx
xx 25 MAR 1997: 2001EP-0204021.
xx
xx 25 MAR 1996: 96EP-0200820.
xx
xx 22 NOV 1996: 96EP-0204284.
xx
xx 25 MAR 1997: 97EP-0200903.
xx
xx (AK01) AK01 NDBEL NV.
xx
xx Mosselman S; Djikema K;
xx
xx W01: 2002 084414/12.
xx
xx N P5008: AA172146.
xx
xx New isolated chimera receptor comprising a DNA binding domain and/or
xx ligand binding domain of a new estrogen receptor, for identifying
xx functional ligands or hormonal analogs for the receptor.
xx
xx Example B: Page 24 25; 45pp; English.
xx
xx The sequences given in AA047846 and AA047847 show splice variants
xx of a novel estrogen receptor (ER). The gene encoding this new ER is
xx located on chromosome 14 and has a different tissue distribution from
xx classical ER. This ER also has two orphan ERs, ER alpha and ER beta.
xx Those orphan receptors have estrogen receptor related structure but do
xx not appear to be able to bind estradiol or other ER ligands. These
xx splice variants differ from the parent ER around exon 8. One clone
xx contains exon 8B through alternative splicing. This causes an immediate
xx termination of the reading thereby creating a truncation at the carboxy
xx terminus. The other splice variant contains an alternative exon 8, exon
xx 8C, which encodes two C-terminal amino acids and then has a stop codon.
xx The splice variant proteins do not contain the AF-2 region and therefore
xx probably lack the ability to modulate transcription of target genes in
xx a ligand dependent manner. However they may be able to interact with
xx the function of the ER classical ER or the novel ER of the invention,
xx either by heterodimerisation or by occupying estrogen response elements
xx or by interactions with other transcription factors.
xx
xx
xx Sequence 418 AA:
xx
xx Query Match: 100.0%; Score 2263; 38 23; Length 418.
xx
xx Host Local Similarity 100.0%; Pred. No. 6, to 202;
xx
xx Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
xx
yy 1 MNSYTSNVNLEKRGKQTSVNVLMPTVHLSPIVVRKLSHYAEKSWCFARSL 60

```

```

|||||
1b 11FAPPLVLDROEGKVEGILEFDMALISPEHELMGHEFVYKAMILLNSMYPL 600
yy 661 VVATVADLSKRKAHLNNAVITATVAVTAKSSISGQOSMRANLMLLSVVRK 416
1b 661 VVATVADLSKRKAHLNNAVITATVAVTAKSSISGQOSMRANLMLLSVVRK 416

RESULT 5
AA047212 standard: protein: 477 AA.
xx AA047212:
xx
xx 20 APR 1998 (first entry)
xx
xx Human estrogen receptor protein.
xx
xx estrogen receptor protein; steroid; alternative splicing; estradiol;
xx estrone; estradiol; screening.
xx
xx Homo sapiens.
xx
xx ER798378-A2.
xx
xx 01 OCT 1997.
xx
xx 25 MAR 1997: 97EP-0200903.
xx
xx 22 NOV 1996: 96EP-0204284.
xx
xx 25 MAR 1997: 96EP-0200820.
xx
xx (AK01) AK01 NDBEL NV.
xx
xx Djikema K; Mosselman S;
xx
xx W01: 1997 47368/44.
xx
xx N P5008: AA184112.
xx
xx DNA encoding estrogen receptor useful in screening assay to
xx identify novel ligands or hormonal analogues
xx
xx (claim 4: Page 18-20; 45pp; English.
xx
xx This sequence represents a novel estrogen binding protein. The cDNA
xx sequence which encodes this protein can be alternatively spliced
xx resulting in the detection of additional transcripts (see AA184112)
xx This receptor is able to bind and be activated by estradiol, estrone and
xx estrone, can be used in a screening assay for the identification of new
xx drugs e.g. novel ligands or hormonal analogues.
xx
xx
xx Sequence 477 AA:
xx

```



```

Query Match 99.8% Score 2198. DB 18 Length 477:
Best Local Similarity: 100.0% Frac. No. 2. Acc 101.
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MNYSPFSVNTNIEGCHQRTSPNVIWPTQSHI SPLVWHPDI SHLVAFPKSHW EAKSL 60
DB 1 MNYSPFSVNTNIEGCHQRTSPNVIWPTQSHI SPLVWHPDI SHLVAFPKSHW EAKSL 60
QY 61 EHTLPVNRKTLKKKSSGKKKASPVIGDPSKKDAHCAVAGSIVASGIVAGWSSGCKAKF 120
DB 61 EHTLPVNRKTLKKKSSGKKKASPVIGDPSKKDAHCAVAGSIVASGIVAGWSSGCKAKF 120
QY 121 KRSLQHNHYTPFAPNMTFHKNPERSQAGPLPKCYFVWVWVKGSPFQVYELVEPQF 180
DB 121 KRSLQHNHYTPFAPNMTFHKNPERSQAGPLPKCYFVWVWVKGSPFQVYELVEPQF 180
QY 181 SAQDQTHCAAGKAPKPSCHAPRVPLIIDAISPVIVITLCAAPRVPLISPAVPLEAS 240
DB 181 SAQDQTHCAAGKAPKPSCHAPRVPLIIDAISPVIVITLCAAPRVPLISPAVPLEAS 240
QY 241 MMSLTKLADKRELHVMISMAKIPGFVEFLSLFDVRLLESQWMEVLMGIMWSIDHPK 300
DB 241 MMSLTKLADKRELHVMISMAKIPGFVEFLSLFDVRLLESQWMEVLMGIMWSIDHPK 300
QY 301 LTFAPDLVLDROGKCVESILETFQMLATTSRERELKIDHREYLVKAMILLNSSMYPL 360
DB 301 LTFAPDLVLDROGKCVESILETFQMLATTSRERELKIDHREYLVKAMILLNSSMYPL 360
QY 461 VTAIQDAISSRKLAHLINAVTALVWVIAKSGISISQOOSMRLANLMLLSHVKHA 415
DB 461 VTAIQDAISSRKLAHLINAVTALVWVIAKSGISISQOOSMRLANLMLLSHVKHA 415

RESULT 6
AAB47834
ID AAB47844 standard; protein: 477 AA.
AC AAB47844:
XX 25-MAR 2002 {first entry}
XX
XX Estrogen receptor.
XX
XX DNA binding domain: DRD; ligand binding domain: LBD; chimeric receptor-
XX estrogen receptor ER- chromosome 14; ER-alpha; ER-beta; exon 8;
XX estradiol; nuclear receptor; progesterone receptor.
XX
XX Homo sapiens.
XX
XX EN F1146244-A2
XX
XX 12-DEC-2001.
XX
XX 25-MAR-1997; 2001EP-0202921.
XX
XX 26-MAR-1996; 96EP-0200820.
XX
XX 22-NOV-1995; 96EP-0202484.
XX
XX 25-MAR-1997; 97EP-0200903.
XX
XX (AIKU ) AKZO NOBEL NV.
XX
XX
XX Mossmann S. Dijkema R;
XX
XX WPI: 2005-084114/12.
XX
XX N-PSIB: AAI72128.
XX
XX New isolated chimeric receptor comprising a DNA binding domain and/or
XX ligand binding domain of a new estrogen receptor, for identifying
XX functional ligands or hormonal analogs for the receptor
XX
XX Example A: Page 15-17; 35pp; English.
XX
XX This sequence shows a novel estrogen receptor (ER). The gene encoding
XX

```

Query	Match	Post local similarity	99.8% Score	2198	DB 24	Length	477
Matches	4157	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MYSTPSNVTNLEGGHGRGTTSPNVIWDPCHSPVIVVRGLSPVYAEPSKSHVFAVSL	60				
DB	1	MYSTPSNVTNLEGGHGRGTTSPNVIWDPCHSPVIVVRGLSPVYAEPSKSHVFAVSL	60				
QY	61	EHITLPNNPPEIIPKPYNSGNPQASPVQYQYSSKQANPQAVNSIVASGVNYVNSVEYKAF	120				
DB	61	EHITLPNNPPEIIPKPYNSGNPQASPVQYQYSSKQANPQAVNSIVASGVNYVNSVEYKAF	120				
QY	121	KPSLQCHNDYIPSPANIGCTTQKNPKKSYGACILKCYEVAQVNGKGSSEFQYPLVRRQR	180				
DB	121	KPSLQCHNDYIPSPANIGCTTQKNPKKSYGACILKCYEVAQVNGKGSSEFQYPLVRRQR	180				
QY	181	SAPDQVQVATKAKKSSGADPVPPEITIALSPSPVLTLEFADPIVLSRPAPPTAS	240				
DB	181	SAPDQVQVATKAKKSSGADPVPPEITIALSPSPVLTLEFADPIVLSRPAPPTAS	240				
QY	241	MMSSLIKLALPELVIMVSWAKTKEFVEVSLFQVPLIFSTVMEVFMGIMKRSIDHPRK	300				
DB	241	MMSSLIKLALPELVIMVSWAKTKEFVEVSLFQVPLIFSTVMEVFMGIMKRSIDHPRK	300				
QY	301	LIFAPRIYLDROGKQVEGILEIFPLMLATTSREPEIKLHKKEYLQKAMILLNSMYPL	360				
DB	301	LIFAPRIYLDROGKQVEGILEIFPLMLATTSREPEIKLHKKEYLQKAMILLNSMYPL	360				
QY	361	VITQVANSRKLALHNLVTPDALVWYIAKSGISQOOSNMLANLIMLSHVHNA	415				
DB	361	VITQVANSRKLALHNLVTPDALVWYIAKSGISQOOSNMLANLIMLSHVHNA	415				

CC intensity in the measured fluorescence. The analyzers are for studying
 CC behaviors of fluorescence-labeled molecules particularly intracellular
 CC biological molecules like proteins at molecular level, e.g. protein
 CC functions and interactions. Such analyzers are stable and convenient to
 CC operate, thereby enabling easy performance of fluorescence correlation
 CC spectroscopy, fluorescence intensity distribution analysis and
 CC fluorescence intensity multiple distribution analysis. The present
 CC sequence represents the amino acid sequence of a fusion protein
 CC comprising a GFP (green fluorescent protein) and hER (human estrogen
 CC receptor) beta protein.

XX
 XX
 SQ Sequence 793 AA:
 Query Match 99.8%; Score 2158; DB 24; Length 793;
 Best Local Similarity 100.0%; Prot. No. 4.7e-201;
 Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYSLPSNVNLEGGHGGPQTTSPNVLWPTPSHSLVWHPQLSHLYAEPSKSPWFAEASL 60
 DB 117 MNYSLPSNVNLEGGHGGPQTTSPNVLWPTPSHSLVWHPQLSHLYAEPSKSPWFAEASL 376
 QY 61 FHTLVNPTETLKPKKVSNGPASPVTGPGSPPAHFVAGSTGYASGYAGVWSYGYKAF 120
 DB 477 FHTLVNPTETLKPKKVSNGPASPVTGPGSPPAHFVAGSTGYASGYAGVWSYGYKAF 436
 QY 121 KRSLGGHNYVTPATNGCTTHKPKKSGACFPRGVFVGVKSGSPFGGYPVPPOR 180
 DB 447 KRSLGGHNYVTPATNGCTTHKPKKSGACFPRGVFVGVKSGSPFGGYPVPPOR 496
 QY 181 SADEQLHCAKAKKPSGAPRVRELLDALSPQLVLTLLAEPPHVLISPSAPFTAS 240
 DB 497 SADEQLHCAKAKKPSGAPRVRELLDALSPQLVLTLLAEPPHVLISPSAPFTAS 556
 QY 241 MMSLTSLKADKELVHMTSMARKIPGVFELSTFDVRLLESQMEVLMKLMKRSIDHPGK 300
 DB 557 MMSLTSLKADKELVHMTSMARKIPGVFELSTFDVRLLESQMEVLMKLMKRSIDHPGK 615
 QY 301 LIFAPDLVLDROGKVEGILEIFDMLLATTSPFELKLGKEYLVKAMILLNSMYPL 360
 DB 617 LIFAPDLVLDROGKVEGILEIFDMLLATTSPFELKLGKEYLVKAMILLNSMYPL 676
 QY 361 VTATGADSSPKRIAHLLNAVTDALVWIAKSGISSQOOSMRLANIMLSHVRA 415
 DB 677 VTATGADSSPKRIAHLLNAVTDALVWIAKSGISSQOOSMRLANIMLSHVRA 741

RESULT 16
 AAY01597
 ID AAY01597 standard; Protein; 485 AA.
 XX
 AC AAY01597:
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DB An estrogen receptor-beta protein.
 XX
 KW differential estrogen receptor; ER-alpha; ER-beta; activation;
 KW API site; therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09911760-A1.
 XX
 PH 11-MAR-1999.
 XX
 PE 41-AUG-1998; 98WO-US18040.
 XX
 PR 04-SEP-1997; 97US-0024708
 XX
 XX (RESO) UNIV CALIFORNIA.
 XX
 XX Gustafsson J., Kuiper GJM, Kushner PJ, Nilsson S,
 PI Isacke K, Stauden TS, Webb P;
 PI

XX
 XX
 DB W01-1999 205173/17.
 DB N-PSDB; AAX2686.
 XX
 XX Screening for test compounds which inhibit or activate estrogen
 PT receptor beta (ER beta) mediated activation at a API site - for use
 PT in therapy
 XX
 PS Claim 14: Page 43-44; 61pp; English.
 XX
 XX The present sequence represents an estrogen receptor-beta. The
 CC specification describes a method for screening test compounds for
 CC differential estrogen receptor (ER) alpha mediated and ER beta-mediated
 CC activation at an API site. The method is used for identifying compounds
 CC which can be used in therapy.

XX
 XX
 SQ Sequence 485 AA:
 Query Match 98.9%; Score 2179; DB 20; Length 485;
 Best Local Similarity 99.4%; Prot. No. 1.5e-199;
 Matches 412; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNYSLPSNVNLEGGHGGPQTTSPNVLWPTPSHSLVWHPQLSHLYAEPSKSPWFAEASL 60
 DB 9 MNYSLPSNVNLEGGHGGPQTTSPNVLWPTPSHSLVWHPQLSHLYAEPSKSPWFAEASL 68
 QY 61 FHTLVNPTETLKPKKVSNGPASPVTGPGSPPAHFVAGSTGYASGYAGVWSYGYKAF 120
 DB 69 FHTLVNPTETLKPKKVSNGPASPVTGPGSPPAHFVAGSTGYASGYAGVWSYGYKAF 128
 QY 121 KRSLGGHNYVTPATNGCTTHKPKKSGACFPRGVFVGVKSGSPFGGYPVPPOR 180
 DB 129 KRSLGGHNYVTPATNGCTTHKPKKSGACFPRGVFVGVKSGSPFGGYPVPPOR 188
 QY 181 SADEQLHCAKAKKPSGAPRVRELLDALSPQLVLTLLAEPPHVLISPSAPFTAS 240
 DB 189 SADEQLHCAKAKKPSGAPRVRELLDALSPQLVLTLLAEPPHVLISPSAPFTAS 248
 QY 241 MMSLTSLKADKELVHMTSMARKIPGVFELSTFDVRLLESQMEVLMKLMKRSIDHPGK 300
 DB 249 MMSLTSLKADKELVHMTSMARKIPGVFELSTFDVRLLESQMEVLMKLMKRSIDHPGK 308
 QY 301 LIFAPDLVLDROGKVEGILEIFDMLLATTSPFELKLGKEYLVKAMILLNSMYPL 360
 DB 309 LIFAPDLVLDROGKVEGILEIFDMLLATTSPFELKLGKEYLVKAMILLNSMYPL 368
 QY 361 VTATGADSSPKRIAHLLNAVTDALVWIAKSGISSQOOSMRLANIMLSHVRA 415
 DB 369 VTATGADSSPKRIAHLLNAVTDALVWIAKSGISSQOOSMRLANIMLSHVRA 423

RESULT 17
 AAW98125
 ID AAW98125 standard; Protein; 549 AA.
 XX
 AC AAW98125:
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DB Mouse estrogen receptor beta isoform mER-beta-1.
 XX
 KW estrogen receptor; ER-beta-1; ER-beta-2; mouse; tumour;
 KW diagnosis; therapy; isoform.
 XX
 OS Mus musculus.
 XX
 PN W09905170-A1.
 XX
 PH 04-FEB-1999.
 XX
 PE 28-JUL-1998; 98WO-US15649.
 XX
 PR 10-JUL-1997; 97US-0054210.
 PR

28 JUN 1997: 970S 005486.0
 XX
 PA (UYVA) UNIV YALE.
 XX
 Location R. Denton R. Calton R. Kischel-Kirton M.
 XX
 W01: 1999 142852/12
 XX
 Human oestrogen receptor beta 4 useful in treating and monitoring
 P1 tumours
 XX
 PS Example 2: Fig 2a: 89pp: English.
 XX
 The present sequence is alternately spliced isoform mkr beta-1
 of the murine complete oestrogen receptor-beta (ER beta-c), or
 mkr beta-1). The mkr beta-1 gene (see AAX24935) contains 9 exons,
 including the newly described exon 5b, which is not found in ER
 beta-1. Exon 5b is located in the ligand binding domain of mkr
 beta-1, and probably plays a significant role in mkr beta-1 function.
 The mkr beta-1 clone was isolated by RT-PCR of mRNA, and by
 amplification from a mouse embryonic stem cell genomic DNA library.
 It lacks exons 5b. Preliminary data indicate that the mkr beta-1
 isoform may be more active than the full-length mkr beta-1 (see
 AAW01281). 2 other isoforms, mkr beta-2 (see AAW0126) and rat ER
 beta-4 (see AAW98127), have also been isolated, and the human exon 5b
 region (see AAX24934) has been identified. Based on these sequences,
 the invention provides methods for identifying agents that block or
 augment ER beta c mediated transcriptional regulation, methods to
 determine whether ER beta c or its isoforms is being expressed in
 tissues or cells, and methods of identifying and using agents that
 block the transcriptional regulation of genes by ER beta c or its
 isoforms, which in turn modulates other biological and pathological
 processes. Gene therapy expression of ER beta-c is envisaged.
 XX
 Sequence 549 AA:
 SQ
 Query Match 90.1%; Score 1985; 108 20; Length 549;
 Host Local Similarity 89.4%; Pred. No. 6, 60; 181;
 Matches 470; Conservative 20; Mismatches 24; Indels 0; Gaps 0.
 1 MNSVLSNVNLEGGDGTSTNVLWPTPSHLSLVVHQSLSHLYAHKSPWFEARSL 60
 73 MNSVSVSTGNEEGVROFASINVLWPTSHLSLHCHGSSLYAHKSPWFEARSL 132
 61 EHTLVNREGLTKRVSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 120
 133 EHTLVNREGLTKRVSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 192
 121 KSTLGHNHYTGATNGCTDKNRKSQVATNKKCYGVWYKGSRRPGYRKVRQR 180
 193 KSTLGHNHYTGATNGCTDKNRKSQVATNKKCYGVWYKGSRRPGYRKVRQR 252
 181 SAEQDLDKAKKRSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 240
 253 SAEQDLDKAKKRSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 312
 241 MMSSTLKADKELVHMTSWAKKIPGVVLSLQVRLLESWMVYLMGLMKRSIDHCK 300
 313 MMSSTLKADKELVHMTSWAKKIPGVVLSLQVRLLESWMVYLMGLMKRSIDHCK 372
 301 LIFAPDVLDRDGRKVEGILEPMLATTSRFEELKQREYLCYVAMILLNSMYPL 360
 373 LIFAPDVLDRDGRKVEGILEPMLATTSRFEELKQREYLCYVAMILLNSMYPL 432
 361 VTAQDADSSKRLAHLLNVAITDAVWVLAQSSQSSQSMRIANLMLSHVRH 414
 433 VTAQDADSSKRLAHLLNVAITDAVWVLAQSSQSSQSMRIANLMLSHVRH 486
 RESULT 18
 AAY044
 ID AAY044 standard: Prototip: 549 AA.
 XX

AAY04444:
 XX
 25 JUN 1999 (first entry)
 XX
 DE Murine mkr beta-1 clone protein sequence.
 XX
 ER Estrogen receptor beta: estrogen receptor beta; ER beta.
 XX
 OS Mus Sp.
 XX
 W09905171 AL.
 XX
 04-FEB-1999.
 XX
 28-JUN-1998: 98W0 US15540.
 XX
 30-JUL-1997: 970S-0054210.
 XX
 28-JUL-1997: 970S-0054869.
 XX
 (UYVA) UNIV YALE.
 XX
 PA Barton R. Chambon P. Denton R. Dupont S. Garriot J.
 XX
 W01: 1999 142853/12.
 XX
 Novel murine oestrogen receptor-beta genes and splice variants -
 P1 useful for treating oestrogen receptor-beta mediated disorders
 XX
 claim 9; Fig 2a: 89pp: English.
 XX
 The present invention describes the murine complete oestrogen receptor
 beta (mkr beta-c) also designated mkr beta-1). The present sequence
 represents mkr beta-1, which is an isoform of mkr beta-c. The protein
 can be used to screen for agents that modulate or block the interaction
 between the ER beta c protein and physiologically, stilbene or
 triphenylethylene (anti)estrogens. The antibody which binds the protein
 can be used in assays to detect activation of the ER beta protein and
 can be used for subcellular localisation of the protein. The
 complementary nucleic acid can be used to inhibit expression of the
 ER beta c nucleic acid.
 XX
 Sequence 549 AA:
 SQ
 Query Match 90.0%; Score 1983; 108 20; Length 549;
 Host Local Similarity 89.1%; Pred. No. 16; 180;
 Matches 469; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
 1 MNSVLSNVNLEGGDGTSTNVLWPTPSHLSLVVHQSLSHLYAHKSPWFEARSL 60
 73 MNSVSVSTGNEEGVROFASINVLWPTSHLSLHCHGSSLYAHKSPWFEARSL 132
 61 EHTLVNREGLTKRVSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 120
 133 EHTLVNREGLTKRVSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 192
 121 KSTLGHNHYTGATNGCTDKNRKSQVATNKKCYGVWYKGSRRPGYRKVRQR 180
 193 KSTLGHNHYTGATNGCTDKNRKSQVATNKKCYGVWYKGSRRPGYRKVRQR 252
 181 SAEQDLDKAKKRSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 240
 253 SAEQDLDKAKKRSQNHASVLTGSKKIDAHCAVSYASGYRGVMSFGCKAPF 312
 241 MMSSTLKADKELVHMTSWAKKIPGVVLSLQVRLLESWMVYLMGLMKRSIDHCK 300
 313 MMSSTLKADKELVHMTSWAKKIPGVVLSLQVRLLESWMVYLMGLMKRSIDHCK 372
 301 LIFAPDVLDRDGRKVEGILEPMLATTSRFEELKQREYLCYVAMILLNSMYPL 360
 373 LIFAPDVLDRDGRKVEGILEPMLATTSRFEELKQREYLCYVAMILLNSMYPL 432
 361 VTAQDADSSKRLAHLLNVAITDAVWVLAQSSQSSQSMRIANLMLSHVRH 414
 433 VTAQDADSSKRLAHLLNVAITDAVWVLAQSSQSSQSMRIANLMLSHVRH 486

10 443 ATASQFASSKRIHINAVTIAVAVISKSSISQSSVPIANIMLISHVPH 495

RESULT 19

AAW14723

ID AAW14723 standard: protein; 485 AA.

XX

XX AAW14723:

XX

01 08-JUN-1997 (first entry)

XX

XX Rat oestrogen receptor beta (ER-beta).

XX

XX Orphan receptor: oestrogen receptor beta; ER-beta;

XX nuclear receptor; prostate cancer, benign prostatic hyperplasia;

XX ovary cancer; cardiovascular disease; osteoporosis;

XX environment, pollutant.

XX

XX Rattus sp.

XX

XX Key Location/Qualifiers

XX FH domain 104..169

XX FT /label= DNA-binding_domain

XX FT domain 259..457

XX FT /label= ligand binding_domain

XX

XX W09709448-A2.

XX

XX 13-MAR-1997.

XX

XX 09-SEP-1996: 96W0-FP03933.

XX

XX 08-MAY-1996: 96GB-0009576.

XX 08-SEP-1995: 95GB-0018272.

XX 15-MAR-1996: 96GB-0005550.

XX 11-APR-1996: 96GB-0007532.

XX

XX (KARO-) KARO Bio AB

XX

XX Ekmart E. Gustafsson J. Kuiper GG:

XX

XX W01: 1997-192842/17.

XX N-PSDB: AAF62842.

XX

XX New isolated oestrogen receptor beta - used to develop prods. for

XX treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular

XX disease

XX

XX Claim 1: Fig 1: 45pp; English.

XX

XX A novel rat orphan receptor (AAW14723) is related to the known

XX oestrogen receptor ER-alpha, and has been designated ER-beta.

XX It is an oestrogen receptor-related nuclear receptor. The ER-beta

XX amino acid sequence was deduced from a cDNA clone (AAF62842) isolated

XX from a rat prostate cDNA library. Rat, human and mouse ER-beta

XX (AAW14723-25) can be used to isolate molecules for use in the

XX treatment of cardiovascular diseases, central nervous system

XX diseases, osteoporosis, prostate or ovarian cancer or benign

XX prostatic hyperplasia and to test environmental chemicals for

XX oestrogenic activity.

XX

XX Sequence 485 AA:

XX

Query Match 89.9% Score 1981 DB 18: Length 485:

Host Local Similarity 89.1% Pred. No. 1,3e-180:

Matches 369: Conservative 20: Mismatches 25: Indels 0: Gaps 0:

QY 1 MNSVTSNVTNLEKGRKQTTSPNVLMTPTGHLSPVLVVRQTSNLYAEFGKSPWCEAFSL 60

DB 9 MNSVTSNVTNLEKGRKQTTSPNVLMTPTGHLSPVLVVRQTSNLYAEFGKSPWCEAFSL 60

QY 61 PHITPVNPFTHKRVSNPQASVPTDPSKPRVAHFVAGCSIVASGYHGVMSCEGCKAF 120

10 69 PHITPVNPFTHKRVSNPQASVPTDPSKPRVAHFVAGCSIVASGYHGVMSCEGCKAF 128

QY 121 KRSIGCHNRYTETATNGTLEKREKRSYVAPELKEVEYMKYSGEPHSGYPLVRQR 180

DB 129 KRSIGCHNRYTETATNGTLEKREKRSYVAPELKEVEYMKYSGEPHSGYPLVRQR 180

QY 181 SAPEQHCACAKRACSGGAPVPEHLLVALSPENVTITCAPPHVITSPQSAPEFAS 240

DB 189 SSSEGVHCLSKAKRNGGAPVPEHLLVALSPENVTITCAPPHVITSPQSAPEFAS 248

QY 241 MMSSTIKLADKELVHMIQAKKIPGVFELSLDQVRLLESIMVEYLMGLMKRSIDHDK 400

DB 249 MMSSTIKLADKELVHMIQAKKIPGVFELSLDQVRLLESIMVEYLMGLMKRSIDHDK 408

QY 361 LIFAPVILPEKGVFSTIFFMDATTSPFPEIKQREKLYVAMILLNSMYPL 460

DB 309 LIFAPVILPEKGVFSTIFFMDATTSPFPEIKQREKLYVAMILLNSMYPL 468

QY 361 VTATQVADSSPKLAHLINAVTIALVAVIAKSSISSQVSMRIANIMLISHVPH 414

DB 369 ASANQFAESSPKRIHLINAVTIALVAVIAKSSISSQVSMRIANIMLISHVPH 422

RESULT 20

AAV01596

ID AAV01596 standard: protein; 485 AA.

XX

XX AAV01596:

XX

XX 17-JUN-1999 (first entry)

XX

XX An oestrogen receptor beta protein.

XX

XX differential oestrogen receptor; ER-alpha; ER-beta; activation;

XX API site; therapy.

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XX Rattus sp.

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XX W09911760-A1.

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XX 11-MAR-1999.

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XX 31-AUG-1998: 98W0-0518040.

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XX 04-SEP-1997: 970S-0923708.

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XX (REGC) UNIV CALIFORNIA.

XX

XX Gustafsson J. Kuiper GGIM, Kushner PJ, Nilsson S:

XX Pach K, Scallan TS, Webb P:

XX

XX W01: 1999-205173/17.

XX N-PSDB: AAX26685.

XX

XX Screening for test compounds which inhibit or activate oestrogen

XX receptor beta (ER-beta) mediated activation at a A1 site - for use

XX in therapy

XX

XX Claim 3: Page 41-43: 61pp; English.

XX

XX The present sequence represents an oestrogen receptor beta. The

XX specification describes a method for screening test compounds for

XX differential oestrogen receptor (ER) alpha-mediated and ER-beta mediated

XX activation at an A1 site. The method is used for identifying compounds

XX which can be used in therapy.

XX

XX Sequence 485 AA:

XX

Query Match 89.9% Score 1981 DB 20: Length 485:

Host Local Similarity 89.1% Pred. No. 1,3e-180:

Matches 469: Conservative 20: Mismatches 25: Indels 0: Gaps 0:

QY 1 MNSVTSNVTNLEKGRKQTTSPNVLMTPTGHLSPVLVVRQTSNLYAEFGKSPWCEAFSL 60


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146 9 MNSVSGESSTNIECHVDELSTSNVNIWTSCHSLAHVPSSTLAVRGGSWWTKAFV 438
147 61 EHLLPVNRETLAKRVSNGASVVDJGSKRAHFAVSDVASTYDVGWSTGGKAF 120
148 69 EHLLPVNRETLAKRVSNGASVVDJGSKRAHFAVSDVASTYDVGWSTGGKAF 128
149 121 KESLGCHNHYDPAWGTTLDRNRKRSQACPLPRVYGVGWKGSRRPFGYRIVRGR 188
150 129 KESLGCHNHYDPAWGTTLDRNRKRSQACPLPRVYGVGWKGSRRPFGYRIVRGR 188
151 181 SADEGLACAKRKSNGASVVDJGSKRAHFAVSDVASTYDVGWSTGGKAF 240
152 189 SSSFGVWRTSKARKNCHAHFVAFELLSLSPGVLLEAFVNVLSRRPFGYRIVRGR 248
153 241 MMSSTLRKAEKELVIMISMAKKDPEVELSLPGVPLPSVGMVIMMSTIMPSDIDR 400
154 249 MMSSTLRKAEKELVIMISMAKKDPEVELSLPGVPLPSVGMVIMMSTIMPSDIDR 408
155 401 LEFAPDLVDRODKVEGELLEFDMLEAFISREKELKDRKRYLVAMILLNSMYPL 360
156 409 LEFAPDLVDRODKVEGELLEFDMLEAFISREKELKDRKRYLVAMILLNSMYPL 368
157 461 VTATGADSSRKLAHLINAVTALVAVTAKSGLSSQGSRMRIANLMLSHVRH 414
158 469 ASADGADSSRKTHLINAATVAVVAVTAKSGLSSQGSRMRIANLMLSHVRH 422
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2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 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2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 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PD 24-JUL-2001.
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 PF 08-NOV-2000: 2000JP-0340097.
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 PE 09-NOV-1999: 99JP-0316113.
 XX
 PA (SOMO) SOMITOMO CHEM CO LTD.
 XX
 DR WPI: 2001-609402/70.
 XX
 DR N-PSDB: AA168126.
 XX
 PT New polypeptide for controlling oestrogen receptor activity comprises
 PT the oestrogen receptor gene.
 XX
 PS Claim 1: Page 23-24; 34pp; Japanese.
 XX
 CC The invention relates to oestrogen receptors and the encoding genes
 CC of the oestrogen receptor genes can be used for evaluating the ability of
 CC controlling oestrogen receptor activity of a chemical substance.
 XX
 SO Sequence 582 AA:
 Query Match 48.8%; Score 1075.5; DB 22; Length 592.
 Best Local Similarity 50.7%; Pred. No. 6,96-94;
 Matches 231; Conservative 65; Mismatches 95; Indels 65; Gaps 12;
 YY 4 YSLP-----SWTNHGGRGRTSPNVIWTRGHSPLVHHQSLHYAEVCKSP 54
 DB 41 YSVPLDAGSPDSGLGSGSP---TSPLVFSSRLSPFM-IPPSHHVLETSIP 94
 YY 54 WCFARSLFHTLPNPFETLKRKVSCKGKASP-----VTCGQSK-----RQAHFVAVSD 101
 DB 95 VRSVSVPSGQGVPRP-----TGCATSEPSYVSGSAGACGCEMAKEMRGVAVSD 146
 YY 102 YASGTHYGVWCEGCKAFKFKRSTGCHNDYITPAINOCTIDNRKSKQARLKRQYVGM 161
 DB 147 YASGTHYGVWCEGCKAFKFKRSTGCHNDYITPAINOCTIDNRKSKQARLKRQYVGM 206
 YY 162 VRCGSPRGGRVIVRQPSA-----DELDHGKAKKRGSGAPR 201
 DB 207 MKRGVKKR-IPVIFETKRPATNIEFKASKI ERYTPGQEPKSSSSACGQSSGSP 265
 YY 202 VRIILLDALSPDQIVLLEAEPRPVILSRP--SAPFTFASMMSTIKLAKELVHIMISW 259
 DB 266 V-----TMSPPQVILLGGAPR-MTCSPTKISPTFTFTMTLTSMAKRELVIHMTW 319
 YY 260 AKKIPGVFI SLFGVRI FSGWVIMMGLMBSIDRPKILFAPDIVDEDEKVEG 319
 DB 320 AKKIPGVFI SLFGVRI FSGWVIMMGLMBSIDRPKILFAPDIVDEDEKVEG 379
 YY 320 IIFETFMIAITSPFEFKIGKRFYCVKAMILENSMYELVTATGQ-ALSSPEIADLN 378
 DB 480 FVETIEMLLATASRRHMLKIKRPFVGLKAILLNSAPSTGTGIMFPLINSKAVVNMID 439
 YY 479 AVTIDALVWIAKSGISSQGSRLANLLMLLSHVRH 414
 DB 440 TITDALLHISQSGSSAQDQSRRAQDILLLSHIRH 475
 RESULT 30
 AAB81600
 ID AAB81600 standard: Protein; 587 AA.
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 AC AAB81600;
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 DT 19-SEP-2002 (first entry)
 XX
 DE Calman oestrogen receptor protein SEQ ID NO:1.
 XX
 KW Calman oestrogen receptor; endocrine disruptor; receptor.
 XX
 OS Calman oestrogen receptor.

PN W0200248360-A1.
 XX
 PD 29-JUN-2002.
 XX
 PE 15-NOV-2001: 2001WO-JP09996.
 XX
 PA (SOMO) SOMITOMO CHEM CO LTD.
 XX
 DR WPI: 2002-557614/59.
 XX
 DR N-PSDB: AB072931.
 XX
 PT Sumida K;
 PT systems for evaluating the ability of chemicals to control estrogen
 PT receptor activity e.g. to assay the safety of chemicals and detecting
 PT endocrine disruptors in environment
 XX
 PS Claim 1: Page 60-63; 81pp; Japanese.
 XX
 CC The present sequence represents an oestrogen receptor isolated from
 CC Calman oestrodinus. The oestrogen receptor gene can be used in testing
 CC systems for evaluating the ability of chemicals to control the
 CC oestrogen receptor activity, e.g. assay safety of chemicals and
 CC detecting endocrine disruptors in environment and the genes and the
 CC DNA are useful in two-hybrid assays
 XX
 SO Sequence 587 AA:
 Query Match 48.8%; Score 1065; DB 24; Length 587;
 Best Local Similarity 52.7%; Pred. No. 7,1e-93;
 Matches 218; Conservative 69; Mismatches 105; Indels 24; Gaps 8;
 YY 22 SPNVIWTRGHSPLVHHR-QLSHYAEVCKSPW--CFARSLFHTLPNPFETLKRKVSQN 78
 DB 100 SPVPLDAGTPDLSPLVHHNSQGVPRYLENDGSGFGMRFAASTFYRP---SADRHLQSK 156
 YY 79 WCFARSLFHTLPNPFETLKRKVSCKGKASP-----VTCGQSK-----RQAHFVAVSD 101
 DB 157 ERMSSTSEKASLSESTKETRYCAVGNVASYGVWCEGCKAFKFKRSTGCHNDYICP 216
 YY 134 ATMOCTIDNRKSKQARLKRQYVGMVGVWCEGCKAFKFKRSTGCHNDYICP 193
 DB 217 ATMOCTIDNRKSKQARLKRQYVGMVGVWCEGCKAFKFKRSTGCHNDYICP 276
 YY 194 RSGGAPRV-RELLD-----ALSPQIVLLEAEPRPVILSRP-SAPFTFASMM 241
 DB 277 TAEIRTPITLMTSLVFKTRKNSPALSTAEQMSALILEAEPDIVSYEDNRPENFASM 336
 YY 242 MKKSTIKLAKFVHIMISWAKKIPGVFI SLFGVRI FSGWVIMMGLMBSIDRPKIL 301
 DB 497 LEAPNILLDPNGSKVEGWHLEPMLATAAFTKMMNIGEEFVTKSTILLNSGVYFL 456
 YY 402 LEAPNILLDPNGSKVEGWHLEPMLATAAFTKMMNIGEEFVTKSTILLNSGVYFL 461
 DB 457 SSTLKSTPEKDVIVVETKIPITPIMAKKSSSTGQSHRPAAITLISHIRH 510
 RESULT 31
 AAG84509
 ID AAG84509 standard: Protein; 595 AA.
 XX
 AC AAG84509;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human oestrogen receptor alpha protein mutant M99V.

or 4-hydroxylamoxifen. The metazoan organism or its cells, such as epidermal cells, hepatocytes or adipocytes, are useful in carrying out a spatiotemporally controlled site-specific recombination of a DNA sequence of interest in its natural chromatin environment. It is also used in screening of medicaments for pathological conditions associated with an alteration of the expression and/or function of the DNA sequence of interest such as skin cancer, inflammation, diabetes, alopecia, obesity, or in promoting hepatic regeneration.

XX Sequence 595 AA:

Query Match 48.1% Score 1063; DB 23; Length 595;

Best Local Similarity 48.7% Pred. No. 1,1e-92;

Matches 219; Conservative 78; Mismatches 99; Indels 54; Gaps 10;

DB 10 TNEGGGRG TTSNVMPTGHSPTLVNKHQSHYAPD 50

DB 76 TGLPYGDSFAAFNSNIGGPPINSVSPLMLLHPPDLSPTLDHGGGVYYLENE 135

DB 51 KSPWC--FARSEHTLVNRPETIKKVSQNPASVLTGQ-----SKDANFVAGSYA 193

DB 136 PSQVTVFPAAPAFVPP--NSINPPQSGSPPLASTNPGSMAMPFAETPVAVNQA 192

DB 104 SYHYGVWSCEGCKAFKFKSTQHNHYTPATNCTIDKNPKSGAGRIKQGVVWVK 163

DB 193 SYHYGVWSCEGCKAFKFKSTQHNHYTPATNCTIDKNPKSGAGRIKQGVVWVK 252

DB 164 GSKRRRCYGLVVRQSANDEHNVAGKRSQGNAPVR-----ELL 207

DB 253 GTHKDPRTYMLKYNRPD-----GGGRFVGSNVMRANIMWSPQMIKFSKNSIA 207

DB 208 DAFSPQVLTLEAFRPLVLSR--PSAPFTASMMSLTDLAEIVHMSKKKTP 265

DB 308 ISTADQWVALIDAPP--LVSEYPTPSPASMMNLTNLADELVHMSKKKTP 266

DB 266 FVELSLFDVRLPSCWVLMVLMKIMRSTIDPKRTIAPDLVDREKVEVSTLEHT 425

DB 367 FVDTLDQVHLLECAMLRLMGLVWRSMENHKKILFAPNLLIDRNGKGVEMVLEFD 426

DB 326 MLATTSPPRELKQIKETGVKAMTILNSMYPLVAT--QDAUSSPKLAILNVAT 484

DB 427 MLATTSPPRMMLDGFPPVCKSTILLNSVYTLSTKSLERKIHIVLITET 496

DB 385 VVVIASQISSQOOSMKLMLLSHVRH 414

DB 487 IHMAKAGILTDQGHQRIADLLISHIEN 516

RESULT 49

AA084507

ID AA084507 standard: Protein: 595 AA

XX AA084507:

XX 10-SEP-2001 (first entry)

XX Human oestrogen receptor alpha protein mutant S409F.

XX Liquid dependent transcriptional factor; oestrogen receptor; PR;

XX glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;

XX MR; peroxisome proliferator-activated receptor protein; PPAR;

XX progesterone receptor protein; PR; pregnane X receptor protein; PXR;

XX thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;

XX transactivation; Eralpha; breast cancer; mutant; mutlein.

XX Homo sapiens.

XX 14-JUN-2001

XX 01-DEC-2000; 2000WU-JP08553.

XX 07 DEC-1999; 99JF-0348022.
 PR 27 DEC-1999; 99JF-0370667.
 PR 07-JUL-2000; 2000JF-0207011.
 PR 21-JUL-2000; 2000JF-0220508.
 PR 02-AUG-2000; 2000JF-0234053.
 PR 03-AUG-2000; 2000JF-0235460.
 PR 03-AUG-2000; 2000JF-0235461.
 PR 03-AUG-2000; 2000JF-0235463.
 XX (SUMO) SUMITOMO CHEM CO LTD.
 XX Saito K, Oike N, Saito H;
 XX WT, 2001 367866/38.

XX Liquid dependent transcriptional factors; nucleic acids encoding them
 PT and cells comprising them and a specified reporter gene, useful for
 XX screening agents for the treatment of breast cancer
 XX Claim 16; Page 174 177; 276pp; English.

XX The present invention relates to liquid dependent transcriptional factors
 CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
 CC receptor protein (GR), mineralocorticoid receptor protein (MR),
 CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
 CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
 CC receptor protein (TR), and vitamin D receptor protein (VDR). The nucleic
 CC acids encoding them and cells comprising them and a specified reporter
 CC gene for the liquid dependent transcriptional factor. These proteins are
 CC useful in the modulation of liquid dependent transcriptional factor
 CC activity. The cells, mutant Eralpha and the polynucleotide encoding it
 CC may be used in assays for qualitatively analysing an activity for
 CC transactivation of a reporter gene by a test Eralpha, for screening
 CC mutant liquid dependent transcriptional factors, for evaluating an
 CC activity for transactivation of a reporter gene by a test Eralpha and/or
 CC for screening a compound useful for treating a disorder of a mutant
 CC Eralpha, especially breast cancer.

XX Sequence 595 AA:

Query Match 48.1% Score 1060; DB 22; Length 595;

Best Local Similarity 48.7% Pred. No. 2.2e-92;

Matches 219; Conservative 77; Mismatches 100; Indels 54; Gaps 10;

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DB 51 KSPWC--FARSEHTLVNRPETIKKVSQNPASVLTGQ-----SKDANFVAGSYA 193

DB 136 PSQVTVFPAAPAFVPP--NSINPPQSGSPPLASTNPGSMAMPFAETPVAVNQA 192

DB 104 SYHYGVWSCEGCKAFKFKSTQHNHYTPATNCTIDKNPKSGAGRIKQGVVWVK 163

DB 193 SYHYGVWSCEGCKAFKFKSTQHNHYTPATNCTIDKNPKSGAGRIKQGVVWVK 252

DB 164 GSKRRRCYGLVVRQSANDEHNVAGKRSQGNAPVR-----ELL 207

DB 253 GTHKDPRTYMLKYNRPD-----GGGRFVGSNVMRANIMWSPQMIKFSKNSIA 407

DB 208 DAFSPQVLTLEAFRPLVLSR--PSAPFTASMMSLTDLAEIVHMSKKKTP 265

DB 308 ISTADQWVALIDAPP--LVSEYPTPSPASMMNLTNLADELVHMSKKKTP 466

DB 266 FVELSLFDVRLPSCWVLMVLMKIMRSTIDPKRTIAPDLVDREKVEVSTLEHT 425

DB 367 FVDTLDQVHLLECAMLRLMGLVWRSMENHKKILFAPNLLIDRNGKGVEMVLEFD 426

DB 326 MLATTSPPRELKQIKETGVKAMTILNSMYPLVAT--QDAUSSPKLAILNVAT 484

DB 427 MLATTSPPRMMLDGFPPVCKSTILLNSVYTLSTKSLERKIHIVLITET 486

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OM protein - protein search, using sw model

Run on: Mon 16, 2003, 13:13:43 : Search time 29.4629 seconds
(without alignments)

598,126 Million cell updates/sec

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Percent score: 2203
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Scoring table:
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Search: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Listing first 120 summaries

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4: /gen2_6/prodata/1/134/5B_COMB.pep.*
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Prod No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	99.8	495	US-08-836-620A-3	Sequence 3, App1
2	2198	99.8	548	US-09-132-619-2	Sequence 1, App1
3	2198	99.8	548	US-09-561-741A-1	Sequence 1, App1
4	2017	91.6	384	US-08-836-620A-15	Sequence 15, App1
5	1981	89.9	484	US-08-836-620A-14	Sequence 14, App1
6	1981	89.9	485	US-08-836-620A-2	Sequence 2, App1
7	1965	89.2	484	US-08-836-620A-14	Sequence 14, App1
8	1965	89.2	485	US-08-836-620A-2	Sequence 2, App1
9	1063	48.3	595	US-08-764-870-12	Sequence 12, App1
10	1063	48.3	595	US-08-980-115-12	Sequence 12, App1
11	1054	47.8	595	US-08-041-986-35	Sequence 35, App1
12	1054	47.8	595	US-08-453-998-2	Sequence 2, App1
13	1052	47.8	591	US-08-836-620A-17	Sequence 17, App1
14	1042	47.3	596	US-08-836-620A-16	Sequence 16, App1
15	1019	46.3	410	5223606	Sequence 16, App1
16	979	44.4	229	US-09-239-642-2	Sequence 2, App1
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18	787	45.7	225	US-08-836-620A-7	Sequence 7, App1
19	655	29.7	773	US-08-564-264-1	Sequence 1, App1
20	621	28.2	651	US-08-693-940-3	Sequence 3, App1
21	621	28.2	651	US-09-566-660-8	Sequence 8, App1
22	621	28.2	651	US-09-040-598-2	Sequence 2, App1
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24	573.5	26.0	458	US-09-141-000-4	Sequence 4, App1
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43	419.5	19.0	525	US-08-764-870-7	Sequence 7, App1
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54	393.5	17.9	462	PCT-US91-00399-2	Sequence 2, App1
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82	344.5	15.6	516	US-08-927-219-141	Sequence 141, App1
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84	342.5	15.5	414	US-08-255-471-9	Sequence 9, App1
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91	341.5	15.5	461	PCT-US95-1352A-2	Sequence 2, App1
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99	341.5	15.5	461	PCT-US95-1352A-2	Sequence 2, App1
100	341.5	15.5	461	PCT-US95-1352A-2	Sequence 2, App1

[illegible]

References

Sequence #: Application US/08/846,620/A
Patent No.: 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: 1.7, MS-DOS 1.05
SOFTWARE: ported in RefToxso #1.0, Version #1.25 (EP0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,620/A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PT/EP96/04944
FILING DATE:
APPLICATION NUMBER: GB 96/18272.1
FILING DATE: 08 SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 96/05540.4
FILING DATE: 15 MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 96/07542.0
FILING DATE: 11 APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 96/09576.5
FILING DATE: 08 MAY-1996
INFORMATION FOR SEQ ID NO.: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IS 08 846,620/A 4

Query Match	73.4%	Score: 2198	Id: 2	Length: 4875
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		II		
1db	9	MNYSPTNNTNLEPDRCTTSPNVAWTPKSLSTLWVHGLSHYATWPKSTWTPAST	60	
UY	61	ETHLVNRELEKRVSGNCAAPVIGPSKRLAHCEWVSLVANSGLYCEWASDECKKAE	120	

128
180
188
240
248
300
308
360
368

Result 1

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05-09-1997-1
1 Sequence 1, Application US/09419617
2 Patent No. 6,22,015
3
4 GENERAL INFORMATION:
5 APPLICANT: WILKINSON, HILARY
6 TITLE OF INVENTION: ESTROGEN RECEPTOR
7 FILE REFERENCE: 20047Y
8 CURRENT APPLICATION NUMBER: US/09/19,617
9
10 CURRENT FILING DATE: 1998-08-25
11 EARLIER APPLICATION NUMBER: 6,058,271
12 EARLIER FILING DATE: 1997-09-08
13 EARLIER APPLICATION NUMBER: 6,050,920
14 EARLIER FILING DATE: 1997-09-30
15 NUMBER OF SEQ ID NOS: 22
16 SOFTWARE: SEQ ID NOS FOR Windows Version 4.0
17
18 SEQ ID NO 1
19
20 TYPE: ORI
21 ORGANISM: HUMAN
22
23 US-09-1997-1

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 $\lambda_{1,m}$

Math. Ch.

50

iii)

54



97

196)

45

iii

9

三

5

(b)

1

QY 461 VTALGATSSRKLAHLNAVTALVWVIAKSSSSSSSMPLANTLMLSHVRA 415
 D6 442 VTATODSSSKLAHLINAVTALVWVIAKSSSSSSSMPLANTLMLSHVRA 486

RESULT 4 US-09-561-741A-1

Sequence 1, Application US/09561741A
 Patent No. 6458551
 GENERAL INFORMATION:
 APPLICANT: WILKINSON, HILARY
 TITLE OF INVENTION: ESTROGEN RECEPTOR
 FILE REFERENCE: 20047Y
 CURRENT APPLICATION NUMBER: US/09/561,741A
 CURRENT FILING DATE: 2000-04-26
 PRIOR APPLICATION NUMBER: 09/139,617
 PRIOR FILING DATE: 1998-08-25
 PRIOR APPLICATION NUMBER: 60/058,271
 PRIOR FILING DATE: 1997-09-08
 PRIOR APPLICATION NUMBER: 60/060,520
 PRIOR FILING DATE: 1997-09-30
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 1
 LENGTH: 548
 TYPE: PRT
 ORGANISM: HUMAN
 US-09-561-741A-1

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 QY 61 EHTLPVNRKTLKRVKSNRCPASPVTPGSKRPAHPCVSDVASTHYVWVSEEGKAF 120
 D6 132 EHTLPVNRKTLKRVKSNRCPASPVTPGSKRPAHPCVSDVASTHYVWVSEEGKAF 191
 QY 121 KRSTGSHNDYICPATNCTIDKNRRKSCACRLKCYEVDWVWVCSREPERCYRFLVROR 180
 D6 192 KRSTGSHNDYICPATNCTIDKNRRKSCACRLKCYEVDWVWVCSREPERCYRFLVROR 251
 QY 181 SADBOLHCAKAKRSGSHAPVRELLDALSPQLVTLLEAPRVYLLISPSAPTEAS 240
 D6 252 SADBOLHCAKAKRSGSHAPVRELLDALSPQLVTLLEAPRVYLLISPSAPTEAS 311
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 D6 312 MMTSITKLADEKELVHMTSMARKTPGVEVLSIFQVAPLLESQWMEVLMGLMPSITROR 371
 QY 401 LIFAPDLVLDRECKCEVGLLEIFDMILATTSFRELKQHKVEYLCVKAMILLNSMYP 360
 D6 472 LIFAPDLVLDRECKCEVGLLEIFDMILATTSFRELKQHKVEYLCVKAMILLNSMYP 431
 QY 461 VTATODSSSKLAHLINAVTALVWVIAKSSSSSSSMPLANTLMLSHVRA 415
 D6 442 VTATODSSSKLAHLINAVTALVWVIAKSSSSSSSMPLANTLMLSHVRA 486

RESULT 4
 US-08-846-620A-15
 Sequence 15, Application US/0884620A
 Patent No. 5958710
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Orphan receptor
 NUMBER OF SEQUENCES: 19
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: WINDOWS-95
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPI)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/846,620A
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP96/03933
 FILING DATE:
 APPLICATION NUMBER: GR 9518272.1
 FILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9605550.4
 FILING DATE: 15-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9607532.0
 FILING DATE: 11-APR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9609576.5
 FILING DATE: 08-MAY-1996
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 384 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-846-620A-15

Query Match 91.64; Score 2017; FR 2; Length 384;
 Best Local Similarity 100.0%; Pred. No. 1,16,214;
 Matches 384; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 QY 93 AHCFAVSDVASTHYVWVSEEGKAFKFSIOGHNDYICPATNCTIDKNRRKSCACRL 152
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 QY 153 LKCYEVDWVWVCSREPERCYRFLVROR SADBOLHCAKAKRSGSHAPVRELLDALSP 212
 D6 122 LKCYEVDWVWVCSREPERCYRFLVROR SADBOLHCAKAKRSGSHAPVRELLDALSP 181
 QY 213 POLVTLLEAPRVYLLISPSAPTEASMMMSITKLADEKELVHMTSMARKTPGVEVLSIF 272
 D6 182 POLVTLLEAPRVYLLISPSAPTEASMMMSITKLADEKELVHMTSMARKTPGVEVLSIF 241
 QY 273 DOVAPLLESQWMEVLMGLMPSITRORLIFAPDLVLDRECKCEVGLLEIFDMILATTS 432
 D6 242 DOVAPLLESQWMEVLMGLMPSITRORLIFAPDLVLDRECKCEVGLLEIFDMILATTS 301
 QY 433 RFRELKQHKVEYLCVKAMILLNSMYPVTATODSSSKLAHLINAVTALVWVIAKSS 392
 D6 402 RFRELKQHKVEYLCVKAMILLNSMYPVTATODSSSKLAHLINAVTALVWVIAKSS 361
 QY 493 ISSQDSMRLANLMLSHVRA 415
 D6 462 ISSQDSMRLANLMLSHVRA 484

RESULT 5
 US-08-846-620A-13
 Sequence 13, Application US/0884620A
 Patent No. 5958710
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Orphan receptor
 NUMBER OF SEQUENCES: 19
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

Empty Match	89.9%	Score 1981	Tab 2	Fourth 483
Post Local Similarity	89.4%	Prod. No. 1.60-210		
Matches	469	Conservation	20	Mismatches 25
		Indels	0	Gaps 0

RESULT 6.
 US 08 046 670A 2
 Sequence 2, Application US/08/046670A
 Patent No. 5988710
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Olfactin receptor
 NUMBER OF SEQUENCES: 19
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS

Query Match	Score	DB	Length
Best Local Similarity	89.18	Prod. No. 1,66	210
Matches 60%, Conservative	20	Mismatches	25
		Indels	0
		Gaps	0

RESULT 7
US OR 836 620A 14
1. INVENTOR: 14, APPLICATION: US200816620A
2. PARENT NO.: 9958110
3. GENERAL INFORMATION:
4. APPLICANT:
5. TITLE OF INVENTION: organ receptor
6. NUMBER OF SEQUENCES: 19
7. COMPUTER READABLE FORM:
8. MEDIUM TYPE: Floppy disk
9. COMPUTER: IBM pc compatible
10. OPERATING SYSTEM: pc DOS/MS-DOS
11. SOFTWARE: Patent in Release #1.0, Version #1.25 (P20)

Query Match: 89.29; Score 1465; E# 2; Length 484;
Best Local Similarity: 88.68; Prod No 9.40-200;
Matches: 367; Conservative: 21; Mismatches: 26; Indels: 0; Gaps: 0;

1 RESULT #
 2 05-08-84 6-620A-5
 3 Sequence 5 Application US/08846620A
 4 Patent No. 5658710
 5 GENERAL INFORMATION:
 6 APPLICANT:
 7 TITLE OF INVENTION: Orphan receptor
 8 NUMBER OF SEQUENCES: 19
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: PatentIn Release #1.0, Version #1.25 (FPO)
 14 CURRENT APPLICATION DATA:

Query Match	89.28	Score	1965	DH	2	Length	485
Best Local Similarity	88.68	Prod. No.	9.4e+09				
Matches	367	Conservative	21	Mismatches	26	Indels	0
				Gaps	0		

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1 RESULT 9
2 US-08-764-870-12
3 Sequence 12, Application US/08764870
4 Patient No. 6246946
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Scanlan, Thomas S
9
10 APPLICANT: Baxter, John D
11
12 APPLICANT: Fletcher, Robert J
13
14 APPLICANT: Wagner, Richard L
15
16 APPLICANT: Kushner, Peter J
17
18 APPLICANT: Apriletti, James W
19
20 APPLICANT: West, Brian
21
22 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
23
24 TITLE OF INVENTION: Binding Domains
25
26 NUMBER OF SEQUENCES: 16

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61 DEK'VEG LEI FOMLATTSKRIFELI ÖKKEYI VAKMILLNSSMYPLASANÓFAESSK 120

191 KUSAFFSILRY - PAMNGI ISQEVILYISSY INKRISVR

171 INDEX


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1 CURRENT ALIGNMENT NUMBER: 05/09/500.654
2 CURRENT FILLING DATE: 2000-02-09
3 EARLIER APPLICATION NUMBER: 9703451.4
4 EARLIER FILLING DATE: 1997-03-17
5 EARLIER APPLICATION NUMBER: 9804289.9
6 EARLIER FILLING DATE: 1998-02-16
7 NUMBER OF SEQ ID NOS: 4
8 SOFTWARE: FASTSEQ for Windows Version 3.0
9 SEQ ID No. 2
10 LENGTH: 458
11 TYPE: PRT
12 ORGANISM: HOMO SAPIENS
13 OS-09-500.654.2
14
15 Query Match
16 Host Local Similarity 26.08; Score 573.5; DB 4; Length 458;
17 Matched 134; Conservative 76; Mismatches 104; Indels 41; Gaps 12;
18
19 73 KVSNSNPASPTGSGSKRD --- AHPAVSNVASYHYGVNSPEYKAPFKRSTQ 125
20 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
21 75 KRLVDSSTIVEDVQKVEYMLNSMRKRLDVGGLASGYHGVNSPEYKAPFKRTQ 134
22 12: 12: 12: 12: 12: 12: 12: 12: 12: 12: 12: 12: 12: 12: 12:
23 126 GHHVYVATNGEITLITNPPFSQAVPLERGVVSMYKQSG---PEYGYRIYKQGSAD 183
24 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13:
25 135 GNLSEYPAINREITFKRRKSSCAQGRKTKVGMKLEGVADLRKQGRYKRRITDE 194
26 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14:
27 184 EQLHCARKKRSKSHAPVPR ELGLDASP EQLVTLFAEPPIVLTSPISAPETAS 240
28 195 -----NSPTINQIVQAKKRPYKIVSILVAREPKIYAMDITVDPDSQK 240
29
30 241 MMSNLRLAKVGLVIMISMAKLEFVHLSTLGVVLLSSVQKVIIMKSLIDGQK 400
31 242 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
32 243 ALPTLIDMLRVLVITMAKRLDEPSTLSAPVMSITLIVGVVPSIPEDE 400
33
34 401 LHPRLVILRQEGVGLVETLEPMALITSPREKTLQHKREYLVKAMILLNS-SMT 459
35 402 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
36 401 LVAVDVIMEDVQSK-LAGLIDNNAITQLVKRYKSKLKEKPEVTLKALALANSMT 458
37 460 LVTATDAUSKSLAHLIN-AVTLDAVWVIAKSGTSSQGSMDLAILMLSHV 413
38 461 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
39 459 ---LEVDVAVQKLVILHVALID---YEAC-QHMEIDPRACKMLMTLLR 402
40
41 RESULT 24
42 HS-09-141-000-4
43 Sequence 4; Application US/09141000
44 Patent No. 6,054,295
45 GENERAL INFORMATION:
46 APPLICANT: Chem. Engg
47 TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
48 FILE REFERENCE: 1999999
49 CURRENT APPLICATION NUMBER: US/09/141.000
50 CURRENT FILLING DATE: 1998-08-26
51 NUMBER OF SEQ ID NOS: 40
52 SOFTWARE: FASTSEQ for Windows Version 3.0
53 SEQ ID No. 4
54 LENGTH: 458
55 TYPE: PRT
56 ORGANISM: Human
57 OS-09-141-000-4
58
59 Query Match
60 Host Local Similarity 26.08; Score 573.5; DB 4; Length 458;
61 Matched 134; Conservative 76; Mismatches 104; Indels 41; Gaps 12;
62
63 73 KVSNSNPASPTGSGSKRD --- AHPAVSNVASYHYGVNSPEYKAPFKRSTQ 125
64 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
65 98 KRLVDSSTIVEDVQKVEYMLNSMRKRLDVGGLASGYHGVNSPEYKAPFKRTQ 157
66
67 126 GHHVYVATNGEITLITNPPFSQAVPLERGVVSMYKQSG---PEYGYRIYKQGSAD 183
68 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13: 13:
69 156 GNLSEYPAINREITFKRRKSSCAQGRKTKVGMKLEGVADLRKQGRYKRRITDE 217
70 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14: 14:

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UY 184 EQLHFGAKKRSQJHAFNR ELIILALSP EQLVITLLEADPHV-LISRSAPETAS 240
DB 218 -----NSRYLNPQIVAPAKFYNKIVSHITVAETFEYVAPETVDFSTIF 264
UY 241 MMMSLTKLAKREIVHISNAKKIPEVHLSIPIQWBLPSYWEPLMELMWSIPIHNRK 400
DB 264 ALTIICDLAPRLVAVIISMAKHIPEFSTISLADQSLQSAAMELITLGVYRSLSTERE 424
UY 401 LIFAPLVLDROGKAVETITFIPLMILATISSEFELKIDREYLVKAMILLNS-SMYP 459
DB 424 IYVADYIMFEPQSK-LASITLNNNAITQIVKYSMTLEFEVTEKALIANANDSMH- 481
UY 460 IYATQDADSSKLAHLIN-AVITDIAVVIYIAKSGIISQDQSPRIANILMLSHV 413
DB 482 -----IEDVAVOKIOLVIEHLDQ-----YEAG-QIHMEDPRACKMLTLPILK 425

RESULT 25
US-09-141-000-6
Sequence 6, Application US/09141000
Patent No. 6054295
GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
FILE REFERENCE: RECEPTOR PROTEINS
FILE REFERENCE: 199909Y
CURRENT APPLICATION NUMBER: US/09/141,000
CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 418
TYPE: PRT
ORGANISM: Human
US-09-141-000-6

Query Match 26.0%; Score 572.5; DB 3; Length 418;
Best local Similarity 39.5%; Pred. No. 1,1e-54;
Matches 126; Conservative 70; Mismatches 90; Indels 42; Gaps 0.

UY 73 KAVSNHFAASPTGSGSKR-----AHFVAVDSYASQYAVQWSELDYKAFKRSQ 125
DB 98 KELYDCSSSTIVEDPQTKCFYMLNSMPKELIYVCGITAGSYGASCEAKKAFKRI 157
UY 126 GANDYICPATNOCITIKNRKKSQACRLKCYEVQVNGSR-PPPGSYLVPPQPSAD 183
DB 158 GNTVSPATNPETIKPPKRSQACAPKMKI KVMQIFGVIPDVPQSPQKYPPTIAE 217
UY 184 EQLHFGAKKRSQJHAFNR ELIILALSP-EQLVITLLEADPHV-LISRSAPETAS 240
DB 218 -----NSRYLNPQIVAPAKFYNKIVSHITVAETFEYVAPETVDFSTIF 264
UY 241 MMMSLTKLAKREIVHISNAKKIPEVHLSIPIQWBLPSYWEPLMELMWSIPIHNRK 400
DB 264 ALTIICDLAPRLVAVIISMAKHIPEFSTISLADQSLQSAAMELITLGVYRSLSTERE 424
UY 401 LIFAPLVLDROGKAVETITFIPLMILATISSEFELKIDREYLVKAMILLNS-SMYP 459
DB 424 IYVADYIMFEPQSK-LASITLNNNAITQIVKYSMTLEFEVTEKALIANANDSMH- 481
UY 460 IYATQDADSSKLAHLIN 378
DB 482 -----IEDVAVOKIOLVIEH 396

RESULT 26
US-09-141-000-2
Sequence 2, Application US/09141000
Patent No. 6054295
GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR

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TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 199909Y
CURRENT APPLICATION NUMBER: US/09/141,000
CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 500
TYPE: PRT
ORGANISM: Human
US-09-141-000-2

Query Match 26.0%; Score 572; DB 3; Length 500;
Best local Similarity 42.1%; Pred. No. 1.7e-54;
Matches 123; Conservative 56; Mismatches 81; Indels 32; Gaps 7;

UY 96 GAVSPYASRYHGWSPGKAKFKRSIQGINVITPAINGCTIDKPPSPYACPIPK 155
DB 103 CLVCGHIASYHGVASQACAKFKRTIQGNIHVSQALINCHITKRRKSCQACRMK 162
UY 166 -YHVSQSK--PEPVYD VVQPSAM-CLFA-KAKSSDIAH-VVPIIILDAI SP 214
DB 163 CLKVMKKEVRLDPVYQSPQRYKRPDLESSPY-----STQISPPA 205
UY 214 CLVITL-----LIFAPHV-LISRSAPETASMMSTLADKELVMS-SMAKIPETV 267
DB 206 KRLTRVSTILVAFKELIYAP-PPQMPEDKALITLQIADPVLVITGMKHIIPS 265
UY 268 ELSPFVPILESQWEVLMMELMWSIIPQSKLHAFQVLPQEDQVEIIEITDM 327
DB 266 SLSLQQLMSLQSAAMELITLGVYRSLSTERYVADYIMDEHSR-LAGLEIYRAI 324
UY 328 LATSSEPELKHREYLVKAMILLNS-SMYPITATQDADSSKLAHLIN 478
DB 325 LQIVRYKKIKVKEFEVITKALIANANDSMV-----IEDVAVOKIOLVIEH 471

RESULT 27
US-08-816-620A-19
Sequence 19, Application US/0883620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatCom in BioCase #1.0, Version #1.25 (EPR)
CURRENT APPLICATION DATA:
AFFI: AIT-25, NMMPK 25, 94, 620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03934
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:

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QY 312 DECKVEGILEIFDMILATSPREELKIOHKEYCVKAMILLNSMPLVAT-QIADSS 476
DB 61 NCKRCVWVFIFDMILATSPREPMNIOGFEFVLEKSLILNSGVYFLSLKLEEK 120
QY 371 RKLHLINAVTALVWVIAKSGISSQOSMPLANILMLSHVRH 414
DB 121 DHHHVPIDKIDTDTIIMMAKAGTIGQCHPRLOLITLSHPR 164

RESULT 40
US-08-836-620A-10
: Sequence 10, Application US/08836620A
: Patient No. 5958710
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Orphan receptor
: NUMBER OF SEQUENCES: 19
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patient Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/836,620A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/97/03933
: FILING DATE:
: APPLICATION NUMBER: GR 9518272.1
: FILING DATE: 08-SEP-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GR 9605550.4
: FILING DATE: 15-MAR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GR 9607542.0
: FILING DATE: 11-APR-1996
: APPLICATION NUMBER: GR 9609576.5
: FILING DATE: 08-MAY-1996
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 243 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
US-08-836-620A-10

Query Match 23.48; Score 519.5; DB 2; Length 243;
Best Local Similarity 56.18; Pred. No. 3,6e-49;
Matches 92; Conservative 45; Mismatches 26; Indels 1; Gaps 1;

QY 252 ELVHMLSWAKKIPFEVLESLFQVRLISCMWEVLMGIMWSIHPRKILFAPDLYDR 311
DB 1 ELVHMLNWKARVGFQDNLNHDVHLLEKAMEILMIGVWMSMKPRKILFAPNILLDR 60
QY 412 DECKVEGILEIFDMILATSPREELKIOHKEYCVKAMILLNSMPLVAT-QIADSS 370
DB 61 NCKRCVWVFIFDMILATSPREPMNIOGFEFVLEKSLILNSGVYFLSLKLEEK 120
QY 371 RKLHLINAVTALVWVIAKSGISSQOSMPLANILMLSHVRH 414
DB 121 DHHHVPIDKIDTDTIIMMAKAGTIGQCHPRLOLITLSHPR 164

RESULT 41
US-08-836-620A-8
: Sequence 8, Application US/08836620A
: Patient No. 5958710
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Orphan receptor

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: NUMBER OF SEQUENCES: 19
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patient Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/836,620A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/99/6703933
: FILING DATE:
: APPLICATION NUMBER: GR 9518272.1
: FILING DATE: 08-SEP-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GR 9605550.4
: FILING DATE: 15-MAR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GR 9607542.0
: FILING DATE: 11-APR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GR 9609576.5
: FILING DATE: 08-MAY-1996
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 243 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: ORIGINAL SOURCE:
: ORGANISM: Rattus rattus
US-08-836-620A-8

Query Match 23.48; Score 515.5; DB 2; Length 243;
Best Local Similarity 55.58; Pred. No. 9,9e-49;
Matches 91; Conservative 45; Mismatches 27; Indels 1; Gaps 1;

QY 252 ELVHMLSWAKKIPFEVLESLFQVRLISCMWEVLMGIMWSIHPRKILFAPDLYDR 311
DB 1 ELVHMLNWKARVGFQDNLNHDVHLLEKAMEILMIGVWMSMKPRKILFAPNILLDR 60
QY 412 DECKVEGILEIFDMILATSPREELKIOHKEYCVKAMILLNSMPLVAT-QIADSS 370
DB 61 NCKRCVWVFIFDMILATSPREPMNIOGFEFVLEKSLILNSGVYFLSLKLEEK 120
QY 371 RKLHLINAVTALVWVIAKSGISSQOSMPLANILMLSHVRH 414
DB 121 DHHHVPIDKIDTDTIIMMAKAGTIGQCHPRLOLITLSHPR 164

RESULT 42
5224606-6
: Patient No. 5224606
: APPLICANT: BLAUDIN DE THE, HUGHES-MARCHIO, AGNES-TIOLLAIS,
: PIPEPPE-BEJEAN, ANNE
: TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR RELATED
: PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
: NUMBER OF SEQUENCES: 11
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/134,130
: FILING DATE: 17-DEC-1987
: PRIOR APPLICATION DATA:
: SEQ ID NO: 6:
: LENGTH: 463
5224606-6

Query Match 20.58; Score 451; DB 6; Length 463;
Best Local Similarity 32.48; Pred. No. 2,6e-41;
Matches 105; Conservative 64; Mismatches 125; Indels 40; Gaps 10;

QY 96 CAVCSRYASVYHGVWMSCECAFAEFKPSIDQENVYGTATNQTTIYHPPKSCVAPLPK 155
DB 1 CIIIGFASGTHGVLTGSCVKVFPAKADQJHNYLIVIRIKRKNTPAQKLRK 60

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[illegible]

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000 74 FERMILH00211055MSMTWVFNQWPSYKRVSGQMIYFADPHINPQPMK FSSFSYSL 798
001 424 F00MLATTSFPRKLIK0REKLYCYKAMLLMS SMTELVATGVDALSSKRLAHLLNAT 481
002 798 GTTMMQHPQFQFQVSEEPFKVKKVLLINTELRKSGTGFPRMSSYIRELKA 855
003 482 DALVWIAKSGTSQDSQSRMLANIC 406
004 456 --IGLRKGVVSSSQRYQLTKL 877
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[illegible]

APPLICATION NUMBER: US 60/008,543
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,606
 FILING DATE: 14-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Jackie N
 REGISTRATION NUMBER: 35,966
 REFERENCE/DOCCKET NUMBER: USAL-246/0105
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)843-5000
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 984 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-764-870-15

Query Match: 19.5%; Score 430.5; DB 4; Length 984;
 Best Local Similarity 41.8%; Prod. No. 2,30,38;

Matches 110; Conservation 59; Mismatch 140; Indels 37; Gaps 9;

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 DB 836 N-ERKHQSAMYELDGMHDSLOVFKQLIFETITKALLIST 880

RESULT 39

US-08-980-115-15
 Sequence 15, Application US/08980115
 Patent No. 6266622
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S.
 APPLICANT: Baxter, John D.
 APPLICANT: Fletchrick, Robert J.
 APPLICANT: Wagner, Richard L.
 APPLICANT: Kushner, Peter J.
 APPLICANT: Apiletti, James W.
 APPLICANT: West, Brian L.
 TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
 FILE REFERENCE: USAL-246/0205
 CURRENT APPLICATION NUMBER: US-08-980,115
 EARLIER FILING DATE: 1997-11-26
 EARLIER APPLICATION NUMBER: 08/764,870
 EARLIER FILING DATE: 1996-12-13
 EARLIER APPLICATION NUMBER: 60/008,606
 EARLIER FILING DATE: 1995-12-14
 EARLIER APPLICATION NUMBER: 60/008,543
 EARLIER FILING DATE: 1995-12-13
 EARLIER APPLICATION NUMBER: 60/008,540

EARLIER FILING DATE: 1995-12-14
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 984
 TYPE: PRI
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: DOMAIN
 LOCATION: (695)..(969)
 OTHER INFORMATION: minimal ligand binding domain
 US-08-980-115-15

Query Match: 19.5%; Score 430.5; DB 4; Length 984;
 Best Local Similarity 41.8%; Prod. No. 2,30,38;

Matches 110; Conservation 59; Mismatch 140; Indels 37; Gaps 9;

QY 40 PQLSHYAFKPSFWFAPSLFHTLPVNP-----ETLKKKVSNGFASVTPVPSKRD 92
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 DB 776 QMTQVVKAKVLPGRKNLPLEDQITLQYSWMCSSFASISWKSXKHNISQFLYAPDLVF 835
 QY 410 DPEKCGEGLIEIFMLATISPEPELKGKEFLCYKAMILNS 355
 DB 836 N-ERKHQSAMYELDGMHDSLOVFKQLIFETITKALLIST 880

RESULT 40

US-08-764-870-13
 Sequence 13, Application US/08764870
 Patent No. 6236946
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S.
 APPLICANT: Baxter, John D.
 APPLICANT: Fletchrick, Robert J.
 APPLICANT: Wagner, Richard L.
 APPLICANT: Kushner, Peter J.
 APPLICANT: Apiletti, James W.
 APPLICANT: West, Brian
 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
 TITLE OF INVENTION: Binding Domains
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Goddard
 STREET: Five Palo Alto Square, 3000 El Camino Real
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER RELEASABLE FROM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICANT: Scanlan, Thomas S.
 FILING DATE: 13-DEC-1996
 CLASSIFICATION: 510


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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 18 DEC 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,544
FILING DATE: 18 DEC 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14 DEC 1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 55,766
REFERENCE/WORK KEY NUMBER: 00/AL-246/2010S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US 08 /64 870 14

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Query Match      19.4% Score 426.5; DB 4; Length 777;
Host Local Similarity 41.6% Prod. No. 4,50-38;
Matches 114; conserved 67; mismatches 133; Indels 45; Gaps 12;

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 Job time: 21.4648 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 16, 2003, 12:15:18 : Search time 45.4127 seconds
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Title: US-08-826-361a-6
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Listing first 120 summaries

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Published Applications-AA:
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 54, April
Sequence 55, April
Sequence 56, April
Sequence 57, April
Sequence 58, April
Sequence 59, April
Sequence 60, April
Sequence 61, April
Sequence 62, April
Sequence 63, April
Sequence 64, April
Sequence 65, April
Sequence 66, April
Sequence 67, April
Sequence 68, April
Sequence 69, April
Sequence 70, April
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Sequence 90, April
Sequence 91, April
Sequence 92, April
Sequence 93, April
Sequence 94, April
Sequence 95, April
Sequence 96, April
Sequence 97, April
Sequence 98, April
Sequence 99, April
Sequence 100, April

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YAHYCKSPWTEAST	60				
YAHYCKSPWTEAST	114				
YAHYCKSPWTEAST	176				
YAHYCKSPWTEAST	240				
YAHYCKSPWTEAST	304				
YAHYCKSPWTEAST	368				
YAHYCKSPWTEAST	432				
YAHYCKSPWTEAST	496				
YAHYCKSPWTEAST	560				
YAHYCKSPWTEAST	624				
YAHYCKSPWTEAST	688				
YAHYCKSPWTEAST	752				
YAHYCKSPWTEAST	816				
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YAHYCKSPWTEAST	944				
YAHYCKSPWTEAST	1008				
YAHYCKSPWTEAST	1072				
YAHYCKSPWTEAST	1136				
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YAHYCKSPWTEAST	1328				
YAHYCKSPWTEAST	1392				
YAHYCKSPWTEAST	1456				
YAHYCKSPWTEAST	1520				
YAHYCKSPWTEAST	1584				
YAHYCKSPWTEAST	1648				
YAHYCKSPWTEAST	1712				
YAHYCKSPWTEAST	1776				
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YAHYCKSPWTEAST	2160				
YAHYCKSPWTEAST	2224				
YAHYCKSPWTEAST	2288				
YAHYCKSPWTEAST	2352				
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YAHYCKSPWTEAST	2480				
YAHYCKSPWTEAST	2544				
YAHYCKSPWTEAST	2608				
YAHYCKSPWTEAST	2672				
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YAHYCKSPWTEAST	4848				
YAHYCKSPWTEAST	4912				
YAHYCKSPWTEAST	4976				
YAHYCKSPWTEAST	5040				
YAHYCKSPWTEAST					

Sequence 2, Appl1	1b	234	SALDGLHFNCRKAFPSCHAPVPELIDALSEGVTLTFAPDQVILSKISAFTHAS	2
Sequence 6, Appl1				
Sequence 2, Appl1	cy	241	MPKSLLEFALPELVMISMAKIFGVESLFLGVGLLESIMVEYIMMLIMKRSIDIRGK	400
Sequence 2, Appl1				
Sequence 2, Appl1	1b	294	MMKSLKTLADKELVIMISMAKIFGVESLFLGVGLLESIMVEYIMMLIMKRSIDIRGK	45
Sequence 2, Appl1				
Sequence 59, Appl1	cy	301	LEFAPDGLVDKDEKCVGLLEFDMLLATTSPFRELKQIHEEYIVKAMLLNSSWPL	460
Sequence 4, Appl1				
Sequence 7, Appl1	1b	454	LEFAPDGLVDKDEKCVGLLEFDMLLATTSPFRELKQIHEEYIVKAMLLNSSWPL	413
Sequence 16, Appl1				
Sequence 20, Appl1	cy	461	VIALTAFASSPKLAHLNAVVTALVWVIAKSSISLQVQSMRLANLMLSHVRIA	415
Sequence 2, Appl1				
Sequence 2, Appl1	1b	414	VIALTAFASSPKLAHLNAVVTALVWVIAKSSISLQVQSMRLANLMLSHVRIA	468
Sequence 18, Appl1				

Sequence 5, Appli

Sequence 11, Appl	Sequence 2, Application for US 09/85,003
Sequence 12, Appl	Patent No. US2002010006A1
Sequence 1, Appl1	GENERAL INFORMATION:
Sequence 2, Appl1	APPLICANT: CHAMON, PIERRE
Sequence 9, Appl1	APPLICANT: METZGER, DANIEL
Sequence 254, Appl	TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
Sequence 3, Appl1	FIELD OF INVENTION: MEDIATED BY MODIFIED CRE-PR
Sequence 2, Appl1	FILE REFERENCE: 06/569,702.2
Sequence 2, Appl1	CURRENT APPLICATION NUMBER: 05/09,785,034
Sequence 2, Appl1	PRIOR FILING DATE: 2001-05-11
Sequence 2, Appl1	PRIOR APPLICATION NUMBER: FR 02/12570
	PRIOR FILING DATE: 2000-10-03
	NUMBER OF SEQ ID NOS: 14
	SOFTWARE: Patent In Vnt, 2.1
	SEQ ID NO: 2
	LENGTH: 595
	TYPE: PR1
	ORGANISM: Homo sapiens
	DN 09 854 034 2

Query Match	48-48	Score 10643	DB 10	Length 5952
Host Local Similarity	48-78	Prod. No. 9,10-862		
Matches 2192	Conservative 767	Mismatches 992	Indels 54	Gaps 102
QY	10	TNLEGGGRQ-----TTSPVLMPTGHSNPLVHROTSHLYAPQ	50	
DB	76	TEHLYGPESEAAATSNLALGPPHNSVSPHMLHPHQQSPHQQHGGQVPPYLENE	145	
QY	81	KSNW---EASLEHLLPVNKEELKPKKSNP---ASVYIGG---SKRAHCAV-SIYA	104	
DB	146	PSGTYVRAAGVATK---NSQKQKQKQKGLASINDKSNMSAKLRYCAVGINYA	192	
QY	104	SGHYGVWSYKAKKAPKRSYGGHNYCTVAINQTIDNRKKSVDALRKKYGVDAWK	164	
DB	194	SGHYGVWSCEPEKAPKRSYGHNYGCVATGCTDNRKRSYDAPLPRGYVDAWK	252	
QY	164	GGSRERQCYVRLVKGROSADEQLACAKKRSCHAPV- - - - -EILL	207	
DB	254	GTTPRPGDQPMKHKRQPR-----GPGKGVKSNQTPKPAANIWSTLMTPEKSNIA	307	
QY	208	DATSTEQVLTLLPAEPHVLISR--PSAPTEASMMSSYTKLAKELVHMLSWAKLPG	265	
DB	308	LSLADQVSLALDAPV--LKYSDYDTPPEASMMGLTLEINLEHVMIMKARVYG	366	
QY	266	FVGLSTPLGVRLSPWMPVIMMIMKRSIDHNGKLPANQVLDHDEKGVGGLLEFD	325	
DB	367	FVGLDNGVGLLPVAMLETLMDGLVWSSHNGKLPANQLLHNGKGVASWVLEFD	426	
QY	325	MLALISPEPKYGRKYLQVAM--LINSNMPLVIAL--QVADSRLANLINVATD	384	
DB	427	MLALISPEPKMNGQCEHVEKSLDLSNGVTPSLSTKSLKEKHQHIVLEDKITPL	486	
QY	385	VWVIAKSTLSGGGSMKLANLMLLSVIG	414	
DB	487	THMKAKALITLGGQGHQALILLISHL	516	


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07  326  MLATTSFPEPLVGFEEFLVAVKAMII NSMPTVAT  GVAAGSPLVAT  TAVATVAT  394
Db  427  MLATSSPPEPMNI  GTEPVVTKSIIIS  VYFLSSLTSLKREKRIHVLRITITL  494
07  485  VWIYAKSGTSSQOOSMRLANIMLMSHVRI  414
Db  487  IIMAKAGITLQOQHORIADQLLLLSHRI  516

RESULT 8
US 10-052-092-9
2 Sequence 9, Applicant US/10052092
3 Publication No. US2004002778A1
4 GENERAL INFORMATION:
5 APPLICANT: Fujita, Suzanne
6 APPLICANT: Allred, D.
7 APPLICANT: Hopp, Torsten A.
8 APPLICANT: O'Connell, Peter
9 TITLE OR INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapies
10 FILE REFERENCE: P0210052
11 CURRENT APPLICATION NUMBER: US/10/052-092
12 PRIORITY FILING DATE: 2002-01-18
13 PRIOR APPLICATION NUMBER: US 60/262,990
14 PRIOR FILING DATE: 2001-01-19
15 PRIOR APPLICATION NUMBER: US 60/304,019
16 PRIOR FILING DATE: 2001-07-09
17 NUMBER OF SEQ ID NOS: 49
18 SOFTWARE: PatentIn version 3.1
19 SEQ ID NO 9
20 LENGTH: 595
21 TYPE: PRT
22 ORGANISM: Human
23 US-10-052-092-9

Query Match          47.88; Score 1054; DB 9; Length 595;
Best Local Similarity 48.48; Pct Id 57.46;
Matches 218; Conservative 78; Mismatches 100; Indels 54; Gaps 10;

07  10  INEGSPRQ-----TSPNLTPTGHSF-LVHRLSHYAPR  50
Db  76  TGLYRGPSFAAFGNSNCLGGEPPLNSVSPFLMLHRRPOLSPFLOHQOVLVYLNE  135
07  51  KSPW--FAKSLFTLLPVNETLKRVNSGASPVTFG-----SPDAHEFVAGSIVA  103
Db  136  PSQTVFAPAPAPAPV---NSGRFGGPERLASINAKGMAKSAFTYCAVCNIVA  192
07  104  SGATYVWASDEGCAFFKRSFGGHNITGATINCTLANKPKSQAELKTEVNSVK  163
Db  193  SGATYVWASFGKAKPKRSFGGHNIVYATNCTIDKPKSCQAPLKREYEVNKK  252
07  164  GGRPRRGVAVLVPKPSANEDQLHCAKSKAKSGHAPV-----RLL  207
Db  253  GGRPRRGVAVLVPKPSANEDQLHCAKSKAKSGHAPV-----RLL  207
07  208  DALSPDVLTLLEAPRHVLSR--PSAPTFASMMNSTKRAKFLVMTSAKKIPG  265
Db  308  LSLADQVNSALDAERP-LIYSEYDTPRESEASSMGLINLADREIVMTNAKRVPG  366
07  266  FVELSLFQVNVLESQNMVEVMGLIMRSIDHPKSLIFAPRLVPRDEGKVEGILEFD  325
Db  367  FVDLTLLHQVHLLEDAVILFIMGLVWPSMEHVRKILFAPRLLDPRNGKVEELMVEFD  426
07  326  MLATTSFPEPLVGFEEFLVAVKAMII NSMPTVAT  GVAAGSPLVAT  TAVATVAT  394
Db  427  MLATSSPPEPMNI  GTEPVVTKSIIIS  VYFLSSLTSLKREKRIHVLRITITL  494
07  485  VWIYAKSGTSSQOOSMRLANIMLMSHVRI  414
Db  487  IIMAKAGITLQOQHORIADQLLLLSHRI  516

RESULT 9

```

US-10-052-092-14
Sequence ID: Affiliation: US-76952092
Publication No.: US200302778A1
GENERAL INFORMATION:
APPLICANT: Futaba, Suzanne
APPLICANT: Allred, D.
APPLICANT: Hopp, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in breast cancer diagnosis and therapy
FILE REFERENCE: P02102082
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,940
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/404,018
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent In version 4.1
SEQ ID NO 13
LENGTH: 595
TYPE: PRI
ORGANISM: human

Query Match 47.8%; Score 1054; DB 9; Length 595;
Best local similarity 48.4%; Pred. No. 5,76-85;
Matches 218; Conservative 78; Mismatches 100; Indels 54; Gaps 10;

GY 10 TNEGGRD-----TSPNLTWTPGLSLP-LVNHGSLHAFQ 50
| | | | | : | | | | |
NB 76 TGLYYGPSEAAAGNSNDLGGFPLNSVPSPLMLHPOLSPFLDHNOGVLYLENE 135
| | | | | : | | | | |
GY KSPWC--EARSLEHTLVNRETLKRVSGNGRCASPVTRG----SKRDHFCAVCSNYA 104
| | | | | : | | | | |
NB 146 PSQTVRAGRPAYRPP---NSDKRGQGRERLASTNRKGSMAMSAKETRYCAVCNYYA 192
| | | | | : | | | | |
GY SCHYVWSSTEGTAFFPESTYGHNIVYCTATNGCTIKKAPSCSW*PIPKCYEVGMVK 164
| | | | | : | | | | |
NB 193 SGYHVWWS*PGTKAEKKSTGCHNVCMYATINCTIIKNPSKYAW*PKIKCYEVGMVK 252
| | | | | : | | | | |
GY GSSPFPGPYAVVROGSADPDLHCACAKKSCSHAVEPR-----ETLI 207
| | | | | : | | | | |
NB 253 GTTRDRDPTGMLKHKRQRD-----GTGRGFVSASDTMPRAANIWDPMIMKRKKNSTA 307
| | | | | : | | | | |
GY 208 DALSPDQVLILAEHPHLISR--PSAPTASMMMSLTKIAKKEIYHIMSAKKIPG 265
| | | | | : | | | | |
NB 308 LSLDAQVSAALDAEP-LLSYEDPTKPEFSASMMLNLINARELVHIMNAKKVPG 366
| | | | | : | | | | |
GY FVELSLFGVALLS*WNEVLMGLMMSIDHRKELLFAFDLYATPRGKVVEELIFTF 325
| | | | | : | | | | |
NB 467 FVDLTLDQVHLLECAMELEIMIGIYWMSMEHVKLLEAFMDLIDPNOKRVEDQVEITFD 426
| | | | | : | | | | |
GY MLATTSFPETKIYKRFVGVKRAMIINSMPVLAIV--PDAPSFKIALIMAAVITAL 484
| | | | | : | | | | |
NB 427 MLATSSFRMNMGTEFEVCLKSILLNSGVYLFSLSLKSLDEMDIHVNLTDIL 486
| | | | | : | | | | |
GY 485 WVVIAKSGISSQOOSMRIANLMLLSHYKH 414
| | | | | : | | | | |
NB 487 IIMAKAGITIOOHORLACOLLISHLRH 516
| | | | | : | | | | |

RESULT 10
US-10-052-092-14
Sequence ID: Affiliation: US-76952092
Publication No.: US200302778A1
GENERAL INFORMATION:
APPLICANT: Futaba, Suzanne
APPLICANT: Allred, D.
APPLICANT: Hopp, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in breast cancer diagnosis and therapy
FILE REFERENCE: P02102082
CURRENT APPLICATION NUMBER: US-10-052-092-14


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Db 76 TGLPYGSGSAAGFSGNGLGPPPLNSVSPRLMLHPPOI:SPFIQHGQGVVYTLNE 135
QY 51 KSIWGC--EARSLEHTLPVNBREILKPKVSGNPGASPYTQJ-----SKRUARPCAVCSUYA 104
Db 136 PSQIVYFAADPAPAFYRP-----NSDNPRGGREPLASTINDGSMAMSAKETPCVAGCINUYA 192
QY 104 SGHYGVWSSGCGKAFKRSIQGHNDYTPDPTNCTIDENPKRSYQACHLKYCYGVNWK 163
Db 193 SGHYGVWSSGCGKAFKRSIQGHNDYTPDPTNCTIDENPKRSYQACHLKYCYGVNWK 252
QY 164 GCSRPFGCYRIYRPSASDPQIHTAGKAKPSGSHAPVP-----EELL 207
Db 254 GCIPIPRGGRMKIKRPPRD-----GPRGPGVSGCIMPANIMSPIM:PRYKXZLA 207
QY 208 DALSPOQVYITIAERPRVYISR--PSAPFTASMMNSITKLAKEIVHMSWAKI1PG 265
Db 408 LSTADQMSALLDAEHP--IIVSEYDTPRFSEASMMGLTINLADRELVHMINAKRVG 366
QY 266 FVETLSLEDOVKELSCMMFVIMMGIIMWRSIDHGRKLEAPDVIYRPRKCYEGILEFD 325
Db 467 FVDLILHDVHLLECAMLEIMGLVWRSNEHVKILFAPNILLDNQKVECHWEI1FD 426
QY 426 MLATTSPPPEIKAFKRYIVVAMTINSSMYETVAT--QVADSEPEIAPINAVTIAI 484
Db 427 MLATSSPPEMMNIGPEFVYKSTIIINSVYTFISSTIKLEFENIHVYLK1T11 484
QY 485 VWIARSGISSQOOSMRILNMLLSVHRH 414
Db 487 IHEMAKAGLTIQOOHRIADLILLISHKH 516

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RESULT 13

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US-10-052-092-31
Sequence: 32 Application: US 7/19/052, 092
Publication No. US2003002778A1
GENERAL INFORMATION:
APPLICANT: Fujita, Suzanne
APPLICANT: Allred, D.
APPLICANT: Hopp, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeu
FILE REFERENCE: P02102052
CURRENT APPLICATION NUMBER: US 7/19/052, 092
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262, 990
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/304, 018
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent In version 3.1
SEQ ID NO 31
LENGTH: 595
TYPE: PRT
ORGANISM: pig
US-10-052-092-31

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Query Match: 47.4%; Score 1045; DB 9; Length 595;

Best Local Similarity 48.0%; Pred. No. 3,60-84;

Matches 217; Conservative 80; Mismatches 97; Indels 56; Gaps 12;

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QY 10 TLEGGPGKQ-----ITSPNWIWPIHQLSP-LVHRLQSLH:YAEPU 50
Db 76 SGIAVFGPSGAAGFSGNGLGPPPLNSVSPRLMLHPPOI:SPFIQHGQGVVYTLNE 135
QY 51 KSIWGC--EARSLEHTLPVNBREILKPKVSGNPGASPYTQJ-----SKRUARPCAVCSUYA 104
Db 146 PSQIVYFAADPAPAFYRP-----NSDNPRGGREPLASTINDGSMAMSAKETPCVAGCINUYA 192
QY 104 SGHYGVWSSGCGKAFKRSIQGHNDYTPDPTNCTIDENPKRSYQACHLKYCYGVNWK 163
Db 193 SGHYGVWSSGCGKAFKRSIQGHNDYTPDPTNCTIDENPKRSYQACHLKYCYGVNWK 252
QY 164 GCSRPFGCYRIYRPSASDPQIHTAGKAKPSGSHAPVP-----EELL 207

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Db 253 GCIPIPRGGRMKIKRPPRD-----GPRGPGVSGCIMPANIMSPIM:PRYKXZLA 207
QY 208 DALSPOQVYITIAERPRVYISR--PSAPFTASMMNSITKLAKEIVHMSWAKI1PG 265
Db 408 LSTADQMSALLDAEHP--IIVSEYDTPRFSEASMMGLTINLADRELVHMINAKRVG 366
QY 266 FVETLSLEDOVKELSCMMFVIMMGIIMWRSIDHGRKLEAPDVIYRPRKCYEGILEFD 325
Db 467 FVDLILHDVHLLECAMLEIMGLVWRSNEHVKILFAPNILLDNQKVECHWEI1FD 426
QY 426 MLATTSPPPEIKAFKRYIVVAMTINSSMYETVAT--QVADSEPEIAPINAVTIAI 484
Db 427 MLATSSPPEMMNIGPEFVYKSTIIINSVYTFISSTIKLEFENIHVYLK1T11 484
QY 485 VWIARSGISSQOOSMRILNMLLSVHRH 414
Db 487 IHEMAKAGLTIQOOHRIADLILLISHKH 516

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RESULT 14

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US-10-052-092-30
Sequence: 32 Application: US 7/19/052, 092
Publication No. US2003002778A1
GENERAL INFORMATION:
APPLICANT: Fujita, Suzanne
APPLICANT: Allred, D.
APPLICANT: Hopp, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeu
FILE REFERENCE: P02102052
CURRENT APPLICATION NUMBER: US 7/19/052, 092
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262, 990
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/304, 018
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patent In version 3.1
SEQ ID NO 30
LENGTH: 595
TYPE: PRT
ORGANISM: hamster
US-10-052-092-30

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Query Match: 47.4%; Score 1044.5; DB 9; Length 595;

Best Local Similarity 49.9%; Pred. No. 40-84;

Matches 211; Conservative 80; Mismatches 105; Indels 27; Gaps 9;

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QY 16 PGQOTSPN--VIMPTGHLSP-LVHRLQSLH:YAEPUKSWCEARSLEHTLPVNBREIL 71
Db 97 POLNSVSPRLMLHPPOI:SPFIQHGQGVVYTLNEPSAVA--VHSIGPAPATRSND 155
QY 72 KPKVSGNPGASPYTQJ-----SKRUARPCAVCSUYA 104
Db 156 NPSQIVYFAADPAPAFYRP-----NSDNPRGGREPLASTINDGSMAMSAKETPCVAGCINUYA 192
QY 127 HNYTGPATNCTIDENPKRSYQACHLKYCYGVNWK 163
Db 216 HNDYTPDPTNCTIDENPKRSYQACHLKYCYGVNWK 252
QY 185 --GLRFAKRSK-----GIAPRVELLIMLSPEQVILIEFPRVVIS 242
Db 276 GRNDQMSALLDAEHP--IIVSEYDTPRFSEASMMGLTINLADRELVHMINAKRVG 366
QY 233 SAFTLASMMNSITKLAKEIVHMSWAKI1PG 265
Db 334 SRFSEASMMNSITKLAKEIVHMSWAKI1PG 265
QY 293 PSIDHGRKLEAPDVIYRPRKCYEGILEFD 325
Db 494 PSMEHGRKLEAPDVIYRPRKCYEGILEFD 325

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Db 789 TIVPALPOLTP--TIVSLIVTPPEVIYACVINSSTPPPTTYSFPAHPPSPASMM 846
 QY 214 GTPV 1A0PT 27
 Db 847 LTNEPEVLYACVSSVSSKGLSSKAHOPFPAALQIKYTTNNSSQVSELDIDABRE 906
 QY 254 VHMISMAKIPGVVELSTFQVVELTSCQVVEVIMMPSIDHCKLTPVQVLDRE 414
 Db 907 VHMINKAKVPPVPPVLTIDVLLVLCAMLETIMGLVWSPSPHPPVLEFAPNILLDRE 966
 QY 314 GQVETLEFEMILATTSPEETKIGHEVLYVAMLLNSMYPVYAT--DANSSPK 372
 Db 967 GKVEPVMVEFEMILATSPFEMMI--GPEFVTKSTITNSVYLTSSITKLPKH 1002
 QY 373 LAHLNATVDALVWIAKSGISSQVSMKAMIMLSHVRH 414
 Db 1027 IIRVITLITLITLIMAKAGILVQVHQLALJLLISHKH 1098

RESULT 18

US-09-908-153B-40
 ? Sequence 40: Application US/09/908153B
 ? Patent No. US2002016871A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Barbas, Carlos F.
 ? APPLICANT: Heerli, Roger
 ? APPLICANT: Schopfer, Ulrich
 ? TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
 ? TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
 ? FILE REFERENCE: ISRI 725.1
 ? CURRENT APPLICATION NUMBER: US/09/908,153B
 ? CURRENT FILING DATE: 2001-07-18
 ? PRIOR APPLICATION NUMBER: US 09/619,064
 ? PRIOR FILING DATE: 2000-07-18
 ? NUMBER OF SEQ ID NOS: 54
 ? SOFTWARE: FastSp for Windows Version 4.0
 ? SEQ ID NO 40
 ? LENGTH: 910
 ? TYPE: PRT
 ? ORGANISM: unknown
 ? OTHER INFORMATION: Synthesized
 US-09-908-153B-40

Query Match: 30.2%; Score 665.5; Db 9; Length 910;
 Host Local Similarity 38.1%; Pred. No. 2,76-50;
 Matches 164; Conservative 76; Mismatches 106; Indels 85; Gaps 17;

QY 47 VVHPOUSHYAPDOKSTWTFASIPHTPVNFETIKPVNSNPPVAFVCTPSTGAPAP 96
 Db 42 LVHGFTHGTEKYPVPP--KSFQSGQKPKH--QKTHPPY FVETVCTG--- 92
 QY 97 AVCSGYA--SGHYG--VMSCEG--KAF-----PKSTGHNHYTCFATNCTIUK 144
 Db 83 SDKRLAKQHPHTDEKPPVAPPPCKSPQSQSHVHPOPTHTGEPYCP--EY----- 144
 QY 144 PPSGACR-----LPKCYGVWVKQSPPEPGYPLVRQSGADPOLHVG 190
 Db 145 -CKSPSPQIAAHGHTHTGEPYCP--KSTSPS-----KLVHQP----- 179
 QY 191 KAKRSGAARVPEFLLD-----ALSPQVITTFAPPP 275
 Db 180 TPKRTSGAPPPHMACTMEAVANIWISPLVTFHTFNSIALSTLAPGWSALDAPD 299
 QY 276 HVLIS-PPSAPPTFASMMSTTKIARKVIMHISMAKIPGVVELSTFQVLLSCME 284
 Db 240 MYSFVPPSPSPASMMSTLNLADPEVHMIMAKRVPVPGGLNHDQVHLDFVAME 299
 QY 285 VIMMIMMPSIDHCKLTPVQVLDREK--VETILEFEMILATSPFELKIGHEV 344
 Db 300 LLMGLVWSPSPHCKLTPAPNILLDRNGKGVBEVLEFDMILATSPFRMNLQGEFF 359

QY 445 VVKAMILLNSMYPVYAT--DQALSPPELHILNATVDALVWIAKSGISSQVSMELA 404
 Db 404 NIMLSHVRH 414
 QY 420 QILLLSHVRH 430

RESULT 19

US-09-908-153B-42
 ? Sequence 42: Application US/09/908153B
 ? Patent No. US2002016871A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Barbas, Carlos F.
 ? APPLICANT: Heerli, Roger
 ? APPLICANT: Schopfer, Ulrich
 ? TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
 ? TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
 ? FILE REFERENCE: ISRI 725.1
 ? CURRENT APPLICATION NUMBER: US/09/908,153B
 ? CURRENT FILING DATE: 2001-07-18
 ? PRIOR APPLICATION NUMBER: US 09/619,064
 ? PRIOR FILING DATE: 2000-07-18
 ? NUMBER OF SEQ ID NOS: 53
 ? SOFTWARE: FastSp for Windows Version 4.0
 ? SEQ ID NO 42
 ? LENGTH: 922
 ? TYPE: PRT
 ? ORGANISM: unknown
 ? OTHER INFORMATION: Synthesized
 US-09-908-153B-42

Query Match: 70.2%; Score 665.5; Db 9; Length 922;
 Host Local Similarity 38.1%; Pred. No. 2,86-50;
 Matches 164; Conservative 76; Mismatches 106; Indels 85; Gaps 17;

QY 47 VVHPOUSHYAPDOKSTWTFASIPHTPVNFETIKPVNSNPPVAFVCTPSTGAPAP 96
 Db 32 LVHGFTHGTEKYPVPP--KSFQSGQKPKH--QKTHPPY FVETVCTG--- 82
 QY 97 AVCSGYA--SGHYG--VMSCEG--KAF-----PKSTGHNHYTCFATNCTIUK 144
 Db 83 SDKRLAKQHPHTDEKPPVAPPPCKSPQSQSHVHPOPTHTGEPYCP--EY----- 144
 QY 144 PPSGACR-----LPKCYGVWVKQSPPEPGYPLVRQSGADPOLHVG 190
 Db 135 -CKSPSPQIAAHGHTHTGEPYCP--KSTSPS-----KLVHQP----- 179
 QY 191 KAKRSGAARVPEFLLD-----ALSPQVITTFAPPP 275
 Db 180 TPKRTSGAPPPHMACTMEAVANIWISPLVTFHTFNSIALSTLAPGWSALDAPD 299
 QY 276 HVLIS-PPSAPPTFASMMSTTKIARKVIMHISMAKIPGVVELSTFQVLLSCME 284
 Db 240 MYSFVPPSPSPASMMSTLNLADPEVHMIMAKRVPVPGGLNHDQVHLDFVAME 299
 QY 285 VIMMIMMPSIDHCKLTPVQVLDREK--VETILEFEMILATSPFELKIGHEV 344
 Db 445 LCVFAMGLNSMYPVYAT--DQALSPPELHILNATVDALVWIAKSGISSQVSMELA 404
 QY 460 VCKLSTILNSGYTTLSTLSKSLKPKHIVYLLKITTLLIMAKAGILVQVH 419
 QY 404 NIMLSHVRH 414
 Db 420 QILLLSHVRH 430

RESULT 20

RESULT 21
 US 09 853 033 B
 Sequence B, Application US/09/853,033
 Patent No. US2002010006A1
 GENERAL INFORMATION:
 APPLICANT: CHAMON, PIERRE
 APPLICANT: METZGER, DANIEL
 TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
 TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
 FILE REFERENCE: 065691/0222
 CURRENT APPLICATION NUMBER: US/09/853,033
 CURRENT FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: FR 00/12570
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 8
 LENGTH: 660
 TYPE: CDS
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Insertion of Artificial Sequence: Chimeric sequence
 OTHER INFORMATION: Homologous bacteriophage p1
 US 09 853 033 B

Query Match	28.68;	Score 640;	DB 10;	Length 660;
Test Local Similarity	56.08;	Prod. NO. 2.50e-47;		
Matches 117;	Conservative	34;	Mistakes	4;
				Gaps 3;

[illegible]

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1 FILE REFERENCE: 11204 004001
2
3 CURRENT APPLICATION NUMBER: US/09/737, 255
4
5 CURRENT FILING DATE: 2000-12-14

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US-10-211-249-1

Query Match 24.58; Score 519.5; DB 9; Length 519;
 Best Local Similarity 38.78; Pred. No. 1,96-39;
 Matches 155; Conservative 50; Mismatches 123; Indels 41; Gaps 9;

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46 46G -----SSTFAFGVAGSTVAGSYVGVWSTGCGVATKESGGRHAGCTVAGN 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
157 AGGAGAGAGCTVTSSTPRCTVAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
147 GATTGKPPKSGVAPPTPEVGVWVKKVSSP--PEFGVPTVPPGAGAG----- 194
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 PFTTKPKPKATVATPTKCTPVMIKEGVLLPVPDGGKPKPKPKPKPKPKPKPKPK 276
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
185 QHWNKAPSGSHAPPELILALSTECVLTLLERHVLISFSAFTTAKKMG 244
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
277 PLAVAGGPKKAPVALVSHLV--VEPEKLV--AMPD-----PAPEDHLLAVAT 323
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
245 FTKEADKEVHMSMAKTPPEVPTSTFVWVLTFTGMVLMWIMMPSTIAPGCTVPA 344
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
324 LQDIDRELVLTISNAKSTPAPSSISLQMSVQLQSVMEVVLVSAGPSLFTQDLATA 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
405 POLVDROGKCVPTITFTIMLATSPRETKTQKPKVLCVAMILLNSMPTVAT 464
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
384 EDVLVD--EGGARAAGLGGELGATLQVPRICATPFREYVLLKALALANSVHI---- 438
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
465 QVADSKRLAHLINAVTALVYVAKSGISSQDSMKLANLLMLLSHVR 413
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
439 EDAAVEQLREALHEA--LLEEGAGAGAGGAGPAPGAPGAPGAPGAPGAPGAPGAP 485
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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RESULT 30
 US-09-864-761-48783

Sequence 48783, Application US/09864761
 Patent No. US20020046763A1

GENERAL INFORMATION:
 APPLICANT: PIONEER BIOLOGICAL
 APPLICANT: KANAK, David R.
 APPLICANT: HANZEL, David K.
 APPLICANT: CHEN, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: ACOmica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: US 60/166,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/757,376
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: CH 242646
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006670

PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonex Sequence List and Engine v0.1.1
 SEQ ID NO: 48783
 LENGTH: 99
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL161756.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL 0.46
 OTHER INFORMATION: SWISSPROT HIT: Q92731, PVALUE 5.00e-52
 OTHER INFORMATION: EST_HUMAN HIT: A1073549.1, PVALUE 2.00e-11
 US-09-864-761-48783

Query Match 22.98; Score 504; DB 10; Length 99;
 Best Local Similarity 100.0%; Pred. No. 2,76-37;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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166 SEPFGVPTVPPGAGAGPQTHGAGKAKRSGSHAPPELITQAI SPQVYVTLPAEP 225
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 SRFGVPTVPPGAGAGPQTHGAGKAKRSGSHAPPELITQAI SPQVYVTLPAEP 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
226 HVLISRPAPPTFASMMSTTKADKEVHMSMAKTP 264
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 HVLISRPAPPTFASMMSTTKADKEVHMSMAKTP 99
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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RESULT 31
 US-10-202-846-2

Sequence 2, Application US/10202846
 Publication No. US2003008447A1

GENERAL INFORMATION:
 APPLICANT: NAGAHAMA, Yoshitaka
 APPLICANT: IKEDUCHI, Yoshitaka
 APPLICANT: KOHAYASHI, Toru
 APPLICANT: TADOKI, Takashi
 TITLE OF INVENTION: PROTEIN-GENE RECEPTOR POLYPEPTIDES, TRANSDUCED CELLS IN WHICH G
 FILE REFERENCE: 113843
 TITLE OF INVENTION: FOR PROTEIN-GENE RECEPTOR POLYPEPTIDES, TRANSDUCED CELLS
 CURRENT FILING DATE: 2002-07-26
 PRIOR APPLICATION NUMBER: JP 2001-235,725
 PRIOR FILING DATE: 2001-08-03
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn version 4.1
 SEQ ID NO: 2
 LENGTH: 689
 TYPE: PRT
 ORGANISM: Anquilla japonica
 US-10-202-846-2

Query Match 20.98; Score 457.5; DB 9; Length 689;
 Best Local Similarity 40.48; Pred. No. 56-32;
 Matches 118; Conservative 72; Mismatches 157; Indels 43; Gaps 12;

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41 GSHVAAEPKSTVAPSTETTLVNPETLKPKVSGPVA-----STVTPGSKPP 92
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
263 KLSLSPSPSSGAGVGLSLSGVHETVYLVCHPNTCHVHNSIKSHVYKMSKSK- 421
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
93 APTCAVSHVASYGVWSPKAPFKKSTGSHNOVYTAIAGCTTAKKPKSVQAKR 152
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
422 --PTLCGPASGSHGVITGSGKVPKVAAPVCHUNTVASRNGTVIVITPRPNFACR 479
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
154 LPTVYVGVKVSPPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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402 LAMLMLSHVR 414
486 FAKLLRLPALR 497

RESULT 49

US-09-965-703-61
Sequence 61: Application US/09965703
Patent No. US2002019521A1
GENERAL INFORMATION:
APPLICANT: Rohm and Haas Company
APPLICANT: Palli, Subba Reddy
APPLICANT: Kapitskaya, Marianna Zinovjevna
APPLICANT: Gress, Dean Evelyn
TITLE OF INVENTION: NO. US2002019521A1-1 Ecdysone Receptor Based Inhibitor Gene Expr
FILE REFERENCE: A010206
CURRENT APPLICATION NUMBER: US/09/965,703
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/2191,355
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/256,799
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: PCT/US01/09050
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentio version 3.1
SEQ ID NO 61
LENGTH: 472
TYPE: PRT
ORGANISM: Choriostoneura fumiferana
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: No. US2002019521A1-1 Sequence
US-09-965-703-61

Query Match 18.78; Score 411.5; DB 10; Length 472;
Best Local Similarity 28.6%; Pred. No. 3,6628;
Matches 120; Conservative 68; Mismatches 136; Indels 95; Gaps 17.

QY 30 CHLSPIVVRHQLSHVAPRQKSP---WCPAPSLPPTLPVNPFTLRKKSCKAPASPVIG 86
DB 72 KQNSPSP-----SPPEKMPDUTAMLDGLDDDTSPNPKNY-----PINH 110
QY 87 P-GSKRDHPCAVGCSYAGYGVWVSCGCKAFKRSIOGHNDYIPPAIQCITDKNR 144
DB 111 PLNSK--HLSICGPRASGRHYGVYSGFRKQPKPTVPKNI SYATPEENQITIDKQ 167
QY 145 KPSQQAHLKCYTFVSKVFGSEFEQNGEIVPELSAEGLECAVAKPSGCHAPVPE 204
DB 168 KNRQYTRVYK-----LACMPPEAVDPEPQSNAPCA-ETAHFSSVAVS----- 212
QY 205 LILDAISPEQVATLEAPPHVILSPSPAPF-----TEANMSLILKLRK 251
DB 214 ---DELSTLR--LIEMIS-----LVAPSEFEQFLKVDGDSNVPKRYAPVSSIDVQGNK 262
QY 252 ELVHMISWARKIPGVHLSLHQVRLLESCWMEVLMGIMKRSIDH----- 297
DB 263 QIALVYVWARDIPHFQILEDDQVLLIKASWELLLEFALVMSMEYLFDERENGITRST 322
QY 298 PKKIFAPRVILDRPCKGVCEHIFTEMLLATS--PPEELKILHRLTYLVKAMILIN 354
DB 323 LQPOLKQIMQKMLHRSAD-QAGVCAIFQVRLSELSIKPPTLPMQAEVAKAVILIN 481
QY 355 SSMPYLVATQDADSSKRIAMINAVTDALVWVAVKSGISSQGSMLANMLLSHVP 414
DB 482 PDVAGLKN-KQFVDVLRK--KMSGLDD-----YGRSRKSNDEGRASILLRLPALR 490

RESULT 40
US-09-922-226-3
Sequence 3: Application US/09922226
Publication No. US2004007766A1
GENERAL INFORMATION:

APPLICANT: Zhao, Yi
APPLICANT: Thacher, Scott M.
APPLICANT: Xiao, Jia-Hao
APPLICANT: Kusari, Jyotirmay
APPLICANT: Chandraratna, Koshantha A.
TITLE OF INVENTION: Methods of Screening for Compounds that
TITLE OF INVENTION: Modulate Hormone Receptor Activity
FILE REFERENCE: P-AR 4681
CURRENT APPLICATION NUMBER: US/09/922,226
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/284,797
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-09-922-226-3

Query Match 18.18; Score 403; DB 9; Length 463;
Best Local Similarity 31.9%; Pred. No. 26,27;
Matches 106; Conservative 53; Mismatches 141; Indels 32; Gaps 8;

QY 83 PVTGSKRDHPCAVGCSYAGYGVWVSCGCKAFKRSIOGHNDYIPPAIQCITDK 142
DB 127 PSTSPGSLVKNHLCAGDRSSGRHYGVYSGFRKQPKPTVPKNI SYATPEENQITIDK 185
QY 143 NPKSQVCPYPRQYVWVYKSGRPEPCYLPVPPSADQLPVAKAPSGHAPV 202
DB 186 KNRQYTRVYKGLVWQMPPEAVQEP-----DPSREAVSEFAPCA-----TSCHDMP 235
QY 203 PELLTALAFQVLTILLAETFIIVLSISAFETASGMSGLTAKELVHMISWAPV 262
DB 236 VERLEA---ELAVEKTESYGDMMENSTNDPVT-----NICHAAKQLEFIVEMAKR 286
QY 263 ITCFVPISTFQVEILFSCWMEVLMGIMKRSIDHNDYIPPAIQCITDKNR 322
DB 287 LPHSPDITLFDQVILLRACWNEILLASFHPSVSGDPIILATGLVHRSRASA-IVGS 345
QY 323 TFDMLLA-TTSREBELKIQHKEYLVKAMILINSSMYPLVATQDADSSKRIANML 381
DB 346 LFDVILIELVSKRKMGMKQKSELGCPALVLENPAAKQSNPSFETLRKVVATLEAVT 405
QY 482 DAVVAVKSGISSQGSMLANMLLSHVP 414
DB 406 KQ-----KYPEPQGFAPKLLRLPALR 427

Search completed: June 16, 2003, 13:41:52
Job time: 46.3127 secs

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•
•

Accession: M41925
 A>Status: significant sequence differences
 A:Molecule type: mRNA
 A:Cross-references: DB:M69296
 A:Experimental source: clone 24, breast cancer
 A:Note: sequence extracted from NBT1 backbone (NCBI:106597)
 C:Comment: The steroid hormones and their receptors are involved in the regulation of complex processes in the absence of ligand, steroid hormone receptors are thought to be weakly complexed to the receptor dimer. DNA sequences between 21 and 24 bp distal start site of the gene.
 A:Accession: M41925
 A:Cross-references: DB:M69296
 A:Map position: 6425-16425
 A:Location: 151-244, 244-364, 432-454, 512-524
 C:Superfamily: estrogen receptor, alpha transcription factor, 151-244 bp
 C:Keywords: DNA binding, nuclear, phosphoprotein, steroid hormone receptor, 151-244 bp
 F:1-20/Region: amino terminal (NBT)
 F:121-229/Region: DNA binding *status predicted (DNA)
 F:181-456/Region: alpha transforming protein homology (EPR)
 F:185-205/Region: zinc finger CXXC motif
 F:221-245/Region: zinc finger CXXC motif
 F:300-595/Region: steroid binding *status predicted (STR)
 F:245-405/Region: steroid binding (STR) (predicted) *status predicted (STR)
 Query Match 47.8% Score 1054 DB 1 Length 595
 Best local similarity 48.4% Pred. No. 20-77
 Matches 218: Conservative 78: Mismatches 100: Indels 54: Gaps 100

10 TNEFGVGRQ TSPNWTGCHLSP LVNVEAFKGVW 55
 11 TNEFGVGRQ TSPNWTGCHLSP LVNVEAFKGVW 55
 12 TNEFGVGRQ TSPNWTGCHLSP LVNVEAFKGVW 55
 13 TNEFGVGRQ TSPNWTGCHLSP LVNVEAFKGVW 55
 14 TNEFGVGRQ TSPNWTGCHLSP LVNVEAFKGVW 55
 15 TNEFGVGRQ TSPNWTGCHLSP LVNVEAFKGVW 55
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Accession: M41925
 A>Status: significant sequence differences
 A:Molecule type: mRNA
 A:Cross-references: DB:M69296
 A:Experimental source: clone 24, breast cancer
 A:Note: sequence extracted from NBT1 backbone (NCBI:106597)
 C:Comment: The steroid hormones and their receptors are involved in the regulation of complex processes in the absence of ligand, steroid hormone receptors are thought to be weakly complexed to the receptor dimer. DNA sequences between 21 and 24 bp distal start site of the gene.
 A:Accession: M41925
 A:Cross-references: DB:M69296
 A:Map position: 6425-16425
 A:Location: 151-244, 244-364, 432-454, 512-524
 C:Superfamily: estrogen receptor, alpha transcription factor, 151-244 bp
 C:Keywords: DNA binding, nuclear, phosphoprotein, steroid hormone receptor, 151-244 bp
 F:1-20/Region: amino terminal (NBT)
 F:121-229/Region: DNA binding *status predicted (DNA)
 F:181-456/Region: alpha transforming protein homology (EPR)
 F:185-205/Region: zinc finger CXXC motif
 F:221-245/Region: zinc finger CXXC motif
 F:300-595/Region: steroid binding *status predicted (STR)
 F:245-405/Region: steroid binding (STR) (predicted) *status predicted (STR)
 Query Match 47.8% Score 1054 DB 1 Length 595
 Best local similarity 48.4% Pred. No. 20-77
 Matches 218: Conservative 78: Mismatches 100: Indels 54: Gaps 100

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Active Site mapping of the ligand filled C-terminal half of the porcine estradiol A
 A: accession number: S66250; MIMD:95461877; PMID:765164
 A: molecule type: protein
 A: residues: 297-607; 410-414; 429-429; 442-442; 443-443; 444-444; 445-445; 446-446; 447-447; 448-448; 449-449; 450-450; 451-451; 452-452; 453-453; 454-454; 455-455; 456-456; 457-457; 458-458; 459-459; 460-460; 461-461; 462-462; 463-463; 464-464; 465-465; 466-466; 467-467; 468-468; 469-469; 470-470; 471-471; 472-472; 473-473; 474-474; 475-475; 476-476; 477-477; 478-478; 479-479; 480-480; 481-481; 482-482; 483-483; 484-484; 485-485; 486-486; 487-487; 488-488; 489-489; 490-490; 491-491; 492-492; 493-493; 494-494; 495-495; 496-496; 497-497; 498-498; 499-499; 500-500; 501-501; 502-502; 503-503; 504-504; 505-505; 506-506; 507-507; 508-508; 509-509; 510-510; 511-511; 512-512; 513-513; 514-514; 515-515; 516-516; 517-517; 518-518; 519-519; 520-520; 521-521; 522-522; 523-523; 524-524; 525-525; 526-526; 527-527; 528-528; 529-529; 530-530; 531-531; 532-532; 533-533; 534-534; 535-535; 536-536; 537-537; 538-538; 539-539; 540-540; 541-541; 542-542; 543-543; 544-544; 545-545; 546-546; 547-547; 548-548; 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A: Genes/loci:
A: Introns: 400/23 451/31 460/3 501/31 533/32 683/31 735/3
C: Superfamily: progesterone receptor; epba transforming protein homology
C: Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
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Db 346 GPEAPADSLPTSAAPRGLYPLGLNGHQAIGPFAVALKELGDPQLCPRLGLYRPDTE- 404
QY 54 WCEARSLPHLTIPVNPETLKRKVSNGNCAAPVTPGSPSKRDAIFGCAVSGYAGYAGWSC 113
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QY 114 EGSKAPRPKPSLTQHINITYICPATNYCTTIRKPKRSCQALRECYEYVNAKQSGPPKCG- 1727
Db 439 GSGKRVKPEKRPMPQDHYITACBPNDITVLRKPKRNPAPRLPKQCAVXVLDGPPKRLNK 498
QY 173 VPIVPPQPSNPTGPIHACQKAKKPSGSHAPVPELLDAL.....SPELV.....LTLL 223
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Db 545 PGTFPEFVYAGYNTPTPTPSLSTESINHPGGLTGVAKKSLTTPRPHLHITQITLI 604
QY 279 ESMQMEFVIMGILMKRSTIDHPS--KLIFADLVLEDEEK-----CYEGSLHITFMLIA 329
Db 605 QYSMMSLMKVAMKMPSTYKVASQMLYFATVITLITNQPKFSSFFVITPTG-----MAG 666
QY 330 TTSFPEPLKLAHREYLVFVAMTILNNSMYEVLIALQVAMSSK--LAHL;NAVITVALVW 457
Db 657 IPEFVPIVLAQSGPEPLVMAKILITNIPFPIPSQSPQDEMTPTSYPELVAA-----ICL 711
QY 348 IAKSGTSSQDQSMPTANT; 406
Db 712 RQKGVVANSQREYQILIKRM 710

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Matches 117; Conservative 57; Mismatches 155; Indels 40; Gaps 11

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107	470	16.8	111	1	ESR1 SHEEP	P49885 ovls atlas
108	465	16.6	628	1	NK43 RAT	P51179 ratlus noty
109	464	16.5	598	1	NK42_HUMAN	P44474 hemo saplin
110	463.5	16.5	480	1	NK61_HUMAN	Q15406 hemo saplin
111	464	16.5	626	1	NK43_HUMAN	Q12570 hemo saplin
112	462	16.4	598	1	NK41_MOUSE	Q19414 ratlus noty
113	462	16.4	598	1	NK42 RAT	Q07947 ratlus noty
114	461	16.4	598	1	NK42_MOUSE	Q05219 mus musculu
115	459.5	16.3	808	1	EFEB_MOUSE	Q05192 otosophilu
116	456.5	16.2	408	1	HN4G_MOUSE	Q19406 mus musculu
117	451	15.9	465	1	HN4G_MOUSE	P49696 mus musculu
118	451	15.9	465	1	HN4G_RAT	P22449 ratlus noty
119	449.5	15.9	408	1	HN4G_HUMAN	Q14541 hemo saplin
120	447	15.8	560	1	NK52_MOUSE	P45448 mus musculu

ALIGNMENTS

RESULT 1

ESR2_HUMAN

STANDARD:

PRG: 540 AA

AC: 092741: 066048; 066048; 075584; 060702; 060703; 075583; 0910K9;

AC: 090806; 090803;

15 JUL 1999 (Ref: 48, Created)

15 JUL 1999 (Ref: 48, Last sequence update)

16 OCT 2001 (Ref: 40, Last annotation update)

DE: Retinon receptor beta (ER beta).

EN: ESR2 OR NR4A2 OR ESRRA.

OS: Homo sapiens (human).

OR: Borkatol; Metazoa; Chordata; Vertebrata; Euteleostomi;

OR: Mammalia; Eularchia; Primates; Carnivora; Homalidae; Homo.

OX: NCBI TaxID:9606;

11]

SEQUENCE FROM N.A. (ISOFORM BETA-1).

KA MEDLINE 98119878; PubMed 947491;

KA Oyama S., Inoue S., Matsuda T., Hiroi H., Ogino A., Hosoi T.,

KA Ouchi Y., Muramatsu M.;

KA "The complete primary structure of human estrogen receptor beta

KA (ERbeta) and its heterodimerization with ER alpha in vivo and in

KA vitro.";

KA Biochem. Biophys. Res. Commun. 241:122-126(1998).

KA [2]

SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.

KA TISSUE: Testis, and breast;

KA MEDLINE 98002862; PubMed 9666672;

KA Moore L.F., McKee D.D., Stenzel-Krober K., Moore L.B., Jones S.A.,

KA Horne E.L., Su J. D., Kilgus S.A., Lehmann J.M., Willison T.M.;

KA "Cloning and characterization of human estrogen receptor beta

KA isoforms.";

KA Biochem. Biophys. Res. Commun. 247:75-79(1998).

KA [3]

SEQUENCE OF 48 540 FROM N.A. (ISOFORM BETA-1), AND CHARACTERIZATION.

KA TISSUE: Testis;

KA MEDLINE 964548/53; PubMed 8749433;

KA Mosselman S., Polman J., Dijkema R.;

KA "ER beta: identification and characterization of a novel human

KA estrogen receptor.";

KA FEBS Lett. 392:49-53(1996).

KA [4]

SEQUENCE FROM N.A. (IS-6-6M BETA 2/3X), AND CHARACTERIZATION.

KA TISSUE: Testis;

KA MEDLINE 984708; PubMed 967411;

KA Oyama S., Inoue S., Matsuda T., Hiroi H., Hosoi T., Ouchi Y.,

KA Muramatsu M.;

KA "Molecular cloning and characterization of human estrogen receptor

KA beta c: a potential inhibitor of estrogen action in human.";

KA Nucleic Acids Res. 26:4505-4512(1998).

KA [5]

SEQUENCE OF 59 540 FROM N.A. (ISOFORMS BETA 5A AND BETA-6).

KA TISSUE: Endometrium;

KA Brandenburger A.W., Lebowitz D., Taylor R.N., Datto R.B.;

KA Submitted (JUN 1998) To The EMBL/Genbank/DBJ databases.

KN	[6]	SEQUENCE FROM N.A. (ISOFORM BETA-2A).	KN	SEQUENCE OF 1.69 FROM N.A.
KN	TISSUE: ovary;	KN	KA "Cloning and characterization of the estrogen receptor beta gene	
KN	TISSUE: ovary;	KN	KA promoter.";	
KN	TISSUE: ovary;	KN	KA Submitted (JUN 1999) To The EMBL/Genbank/DBJ databases.	
KN	TISSUE: ovary;	KN	KA [8]	
KN	TISSUE: ovary;	KN	KA MEDLINE 97467483; PubMed 9426415;	
KN	TISSUE: ovary;	KN	KA Fave P., Taylor J., Sandharatnag S., Coombes R.C., Ali S.;	
KN	TISSUE: ovary;	KN	KA "Human estrogen receptor beta binds DNA in a manner similar to and	
KN	TISSUE: ovary;	KN	KA dimerizes with estrogen receptor alpha.";	
KN	TISSUE: ovary;	KN	KA J. Biol. Chem. 272:25832-25838(1997).	
KN	TISSUE: ovary;	KN	KA [7]	
KN	TISSUE: ovary;	KN	KA FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF ER	
KN	TISSUE: ovary;	KN	KA ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING	
KN	TISSUE: ovary;	KN	KA ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN DEPENDENT MANNER.	
KN	TISSUE: ovary;	KN	KA ISOFORM BETA-EX LACKS LIGAND BINDING ABILITY AND HAS NO OR ONLY	
KN	TISSUE: ovary;	KN	KA VERY LOW ERE BINDING ACTIVITY RESULTING IN THE LOSS OF LIGAND-	
KN	TISSUE: ovary;	KN	KA DEPENDENT TRANSACTIVATION ABILITY. DNA BINDING BY ER-ALPHA AND	
KN	TISSUE: ovary;	KN	KA BETA IS RAPIDLY LOST AT 47 DEGREES CELSIUS IN THE ABSENCE OF	
KN	TISSUE: ovary;	KN	KA LIGAND WHILE IN THE PRESENCE OF 17 BETA-ESTRADIOL AND 4 HYDROXY	
KN	TISSUE: ovary;	KN	KA TAMOXIFEN LOSS IN DNA BINDING AT ELEVATED TEMPERATURE IS MORE	
KN	TISSUE: ovary;	KN	KA GRADUAL.	
KN	TISSUE: ovary;	KN	KA [9]	
KN	TISSUE: ovary;	KN	KA SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER	
KN	TISSUE: ovary;	KN	KA ALPHA. ISOFORM BETA-2/EX PREFERENTIALLY FORMS A HETERODIMER WITH	
KN	TISSUE: ovary;	KN	KA ER-ALPHA RATHER THAN ER-BETA AND INHIBITS DNA BINDING BY ER ALPHA.	
KN	TISSUE: ovary;	KN	KA [10]	
KN	TISSUE: ovary;	KN	KA ALTERNATIVE PROMOTERS: 8 ISOFORMS: BETA-1 (SHOWN HERE), BETA-2/EX,	
KN	TISSUE: ovary;	KN	KA BETA-2A, BETA-3, BETA-4, BETA-5, BETA-5A AND BETA-6; ARE PRODUCED	
KN	TISSUE: ovary;	KN	KA BY ALTERNATIVE SPLICING.	
KN	TISSUE: ovary;	KN	KA [11]	
KN	TISSUE: ovary;	KN	KA TISSUE SPECIFICITY: ISOFORM BETA-1 IS EXPRESSED IN TESTIS AND	
KN	TISSUE: ovary;	KN	KA OVARY, AND AT A LOWER LEVEL IN HEART, BRAIN, PLACENTA, LIVER,	
KN	TISSUE: ovary;	KN	KA SKELETAL MUSCLE, SPLEEN, THYMUS, PROSTATE, COLON, BONE MARROW,	
KN	TISSUE: ovary;	KN	KA MAMMARY GLAND AND UTERUS. ALSO FOUND IN UTERINE BONE, BREAST, AND	
KN	TISSUE: ovary;	KN	KA OVARIAN TUBER CELL LINES, BUT NOT IN COLON AND LIVER TUMORS.	
KN	TISSUE: ovary;	KN	KA [12]	
KN	TISSUE: ovary;	KN	KA ISOFORM BETA-2 IS EXPRESSED IN SPLEEN, THYMUS, TESTIS AND OVARY	
KN	TISSUE: ovary;	KN	KA AND AT A LOWER LEVEL IN SKELETAL MUSCLE, PROSTATE, COLON, SPALT,	
KN	TISSUE: ovary;	KN	KA INTERSTINE, LEUKOCYTES, BONE MARROW, MAMMARY GLAND AND UTERUS.	
KN	TISSUE: ovary;	KN	KA [13]	
KN	TISSUE: ovary;	KN	KA ISOFORM BETA-3 IS FOUND IN TESTIS. ISOFORM BETA-4 IS EXPRESSED IN	
KN	TISSUE: ovary;	KN	KA TESTIS, AND AT A LOWER LEVEL IN SPLEEN, THYMUS, OVARY, MAMMARY	
KN	TISSUE: ovary;	KN	KA GLAND AND UTERUS. ISOFORM BETA-5 IS EXPRESSED IN TESTIS, PLACENTA,	
KN	TISSUE: ovary;	KN	KA SKELETAL MUSCLE, SPLEEN AND LEUKOCYTES, AND AT A LOWER LEVEL IN	
KN	TISSUE: ovary;	KN	KA HEART, LUNG, LIVER, KIDNEY, PANCREAS, THYMUS, PROSTATE, COLON,	
KN	TISSUE: ovary;	KN	KA SMALL INTESTINE, BONE MARROW, MAMMARY GLAND AND UTERUS, NOT	
KN	TISSUE: ovary;	KN	KA EXPRESSED IN BRAIN.	
KN	TISSUE: ovary;	KN	KA [14]	
KN	TISSUE: ovary;	KN	KA DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,	
KN	TISSUE: ovary;	KN	KA A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	
KN	TISSUE: ovary;	KN	KA [15]	
KN	TISSUE: ovary;	KN	KA STIMULATORY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.	
KN	TISSUE: ovary;	KN	KA [16]	

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DR	EMBL: AF061055; AAC49785.1;
DR	EMBL: AF060555; AAC15244.1;
DR	EMBL: X91012; CAA67555.1; ALT: INT1.
DR	EMBL: AB006589; JAA24966.1;

[illegible][illegible]

[illegible]

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18  HSSD; P03372; HCG.
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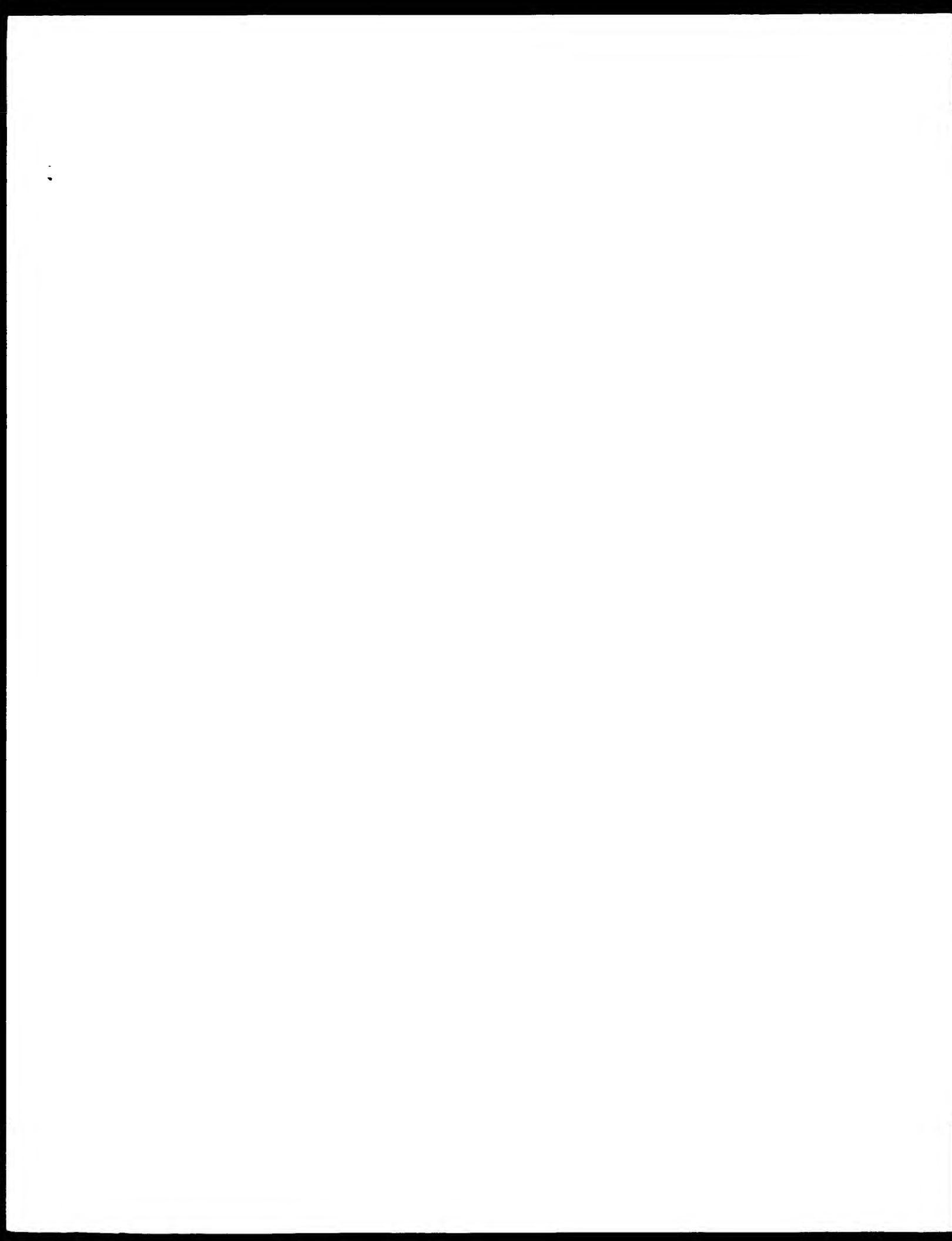
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R¹ TISSUE (vary):
 KX MEDLINE: 20218982; PubMed: 10753576;

256 MISCARRIED PREGNANTIES AND THE RISK OF SUBSEQUENT SPONTANEOUS ABORTION 415

PA Pfeiffer H., Fucini F., Castagnella L., Vidali G.:
 KI "Estrogen receptor variant messenger RNA lacking exon 4 in estrogen
 KI responsive human breast cancer cell lines."
 KI *Cancer Res.* 53:741-744(1993).
 KI [64]
 RP SEQUENCE OF 110-117. PHOSPHORYLATION, AND MUTAGENESIS.
 RX MEDLINE=96036469; PubMed=7476978;
 KA Joel P.B., Traish A.M., Lannigan D.A.:
 KI "Estradiol and phorbol ester cause phosphorylation of serine 118 in
 KI the human estrogen receptor."
 KI *Mol. Endocrinol.* 9:1041-1052(1995).
 KI [7]
 RP SEQUENCE OF 354-548 FROM N.A.
 RP TISSUE-BREAST CARCINOMA.
 RA Naundorf H., Becker M., Fiebig C., Buettner B., Fichtner I.:
 KI "Mechanisms of acquired tamoxifen resistance in a xenotransplanted
 KI human breast carcinoma."
 KI Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases
 KI [8]
 RP SEQUENCE OF 413-595 FROM N.A.
 RP PARKER A.:
 KI Submitted (APR-2000) to the EMBL/GenBank/DBJ databases
 KI [9]
 RP SEQUENCE OF 532-542, AND PHOSPHORYLATION.
 RX MEDLINE=95280953; PubMed=7539106;
 KA Arnold S.F., Choum J.D., Jaffe H., Notides A.C.:
 KI "Phosphorylation of the human estrogen receptor on tyrosine 537 in
 KI vivo and by src family tyrosine kinases in vitro."
 KI *Mol. Endocrinol.* 9:24-33(1995).
 KI [10]
 RP PHOSPHORYLATION.
 RX MEDLINE=95149025; PubMed=7838153;
 KA Arnold S.F., Choum J.D., Jaffe H., Notides A.C.:
 KI "Serine 167 is the major estradiol-induced phosphorylation site on the
 KI human estrogen receptor."
 KI *Mol. Endocrinol.* 8:1208-1214(1994).
 KI [11]
 RP PHOSPHORYLATION OF SER-104 AND SER-106, AND MUTAGENESIS.
 RX MEDLINE=95357754; PubMed=10428798;
 KA Kozlarsky L., Trowbridge J.M., Garabedian M.J.:
 KI "Potential role of human estrogen receptor alpha transcriptional
 KI activation through phosphorylation of serines 104 and 106 by the
 KI cys-1 in A-CDK2 complex."
 KI *J. Biol. Chem.* 274:22296-22302(1999).
 KI [12]
 RP STRUCTURE BY NMR OF 180-262.
 RX MEDLINE=91061891; PubMed=2247153;
 KA Schwabe J.W.E., Neuhans D., Rhodes D.:
 KI "Solution structure of the DNA-binding domain of the estrogen
 KI receptor."
 KI *Nature* 448:458-461(1990).
 KI [13]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 180-262.
 RX MEDLINE=94037103; PubMed=9348790;
 KA Schwabe J.W.E., Chapman L., Finch J.L., Rhodes D.:
 KI "The crystal structure of the estrogen receptor DNA-binding domain
 KI bound to DNA: how receptors discriminate between their response
 KI elements."
 KI *Cell* 75:567-578(1993).
 KI [14]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.
 RX MEDLINE=97478539; PubMed=9348790;
 KA Hozosowski A.M., Pike A.C.W., Dauter Z., Hubbard R.E., Roun J.:
 KI "First structure of estrogen receptor: a dimeric protein with a
 KI molecular basis of agonism and antagonism in the estrogen
 KI receptor."
 KI *Nature* 389:753-758(1997).
 KI [15]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 306-544.
 RX MEDLINE=98261297; PubMed=9600906;
 KA Jancbaum D.M., Ward Y., Williams S.P., Sigler P.B.:
 KI "Crystallographic comparison of the estrogen and progesterone
 KI receptor's ligand binding domains."

KL *Proc. Natl. Acad. Sci. U.S.A.* 95:5996-6003(1998).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 264-554.
 RX MEDLINE=99091051; PubMed=9875847;
 KA Shih A.K., Barstad D., Loria P.M., Cheng L., Kushner P.J.:
 RA Agard D.A., Greene G.L.:
 KI "The structural basis of estrogen receptor/coactivator recognition
 KI and the antagonism of this interaction by tamoxifen."
 KI *Cell* 95:927-937(1998).
 KI [17]
 RP 3D-STRUCTURE MODELING OF 411-547.
 RX MEDLINE=98280806; PubMed=9619507;
 KA Maloni G.J., Xu W., Smith T., Mohr S.C.:
 KI "Homology model for the ligand-binding domain of the human estrogen
 KI receptor."
 KI *J. Biomol. Struct. Dyn.* 15:841-850(1998).
 KI [18]
 RP VARIANT VAL-400.
 RX MEDLINE=9005402; PubMed=2792078;
 KA Tora L., Mullick A., Metzger D., Pandikidakis M., Park I.:
 RA Chambon P.:
 KI "The cloned human estrogen receptor contains a mutation which alters
 KI its hormone binding properties."
 KI *EMBO J.* 8:1981-1986(1989).
 KI [19]
 RP VARIANT ALA-447.
 RX MEDLINE=92259550; PubMed=1577818;
 KA Reese J.C., Katzenellenbogen B.S.:
 KI "Characterization of a temperature-sensitive mutation in the hormone
 KI binding domain of the human estrogen receptor. Studies in cell
 KI extracts and intact cells and their implications for
 KI hormone-dependent transcriptional activation."
 KI *J. Biol. Chem.* 267:9868-9873(1992).
 KI [20]
 RP VARIANT GLU-464.
 RX MEDLINE=97120591; PubMed=8961462;
 KA McInerney E.M., Ince B.A., Shapiro D.J., Katzenellenbogen B.S.:
 KI "A transcriptionally active estrogen receptor mutant is a novel type
 KI of dominant negative inhibitor of estrogen action."
 KI *Mol. Endocrinol.* 10:1519-1526(1996).
 KI [21]
 RP VARIANT CYS-160.
 RX MEDLINE=97346667; PubMed=9195227;
 KA Anderson T.L., Wooster R., Laake R., Collins N., Warren W., Skrede M.:
 RA Feles R., Twill K.M., Johnston S.R.D., Dowsett M., Olsen A.O.:
 KI "Screening for ESR mutations in breast and ovarian cancer patients."
 KI *Hum. Mutat.* 9:531-536(1997).
 KI [22]
 RP FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 KI THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 KI PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC [23]
 RP FUNCTION: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 KI BETA.
 CC [24]
 RP SUBCELLULAR LOCATION: Nuclear.
 CC [25]
 RP ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC [26]
 RP DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC [27]
 RP DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC [28]
 RP PHOSPHORYLATED BY CYCLIN A/CDC2. PHOSPHORYLATION PROBABLY
 CC ENHANCES TRANSCRIPTIONAL ACTIVITY.
 CC [29]
 RP MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS
 CC ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;
 CC HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE
 CC HORMONE RECEPTOR COMPLEX ALTERS TO REDUCE DISCRETE DNA
 CC SEQUENCES, PREPARE OF TRANSCRIPTIONAL START SITES.
 CC [30]
 RP SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC [31]
 RP NBS SUBFAMILY.
 CC [32]
 RP THIS SWISS PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial



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EM protein - protein search, using sw model

Run on: June 16, 2003, 11:34:03 : Search time 23.9719 seconds
(without alignments)

3575, 671 Million cell updates/sec

Title: US-08-826-361a-6

Perfect score: 2203

Sequence: 1 MMSIPSNVTNFKKPSPT

COSMIDAM1.M1SHVHPAP 41c

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 120 summaries

Database:

SPRMBM_21:
1: SP archaea:
2: SP bacteria:
3: SP fungi:
4: SP human:
5: SP invertebrate:
6: SP mammal:
7: SP mhc:
8: SP organell:
9: SP phage:
10: SP plant:
11: SP rodent:
12: SP virus:
13: SP vertebrate:
14: SP unclassified:
15: SP virus:
16: SP bacteriap:
17: SP archaeap:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	97.2	499	6	Q95MFO mouse art
2	2058	93.4	486	6	Q95MFO mouse art
3	1989	88.9	503	11	Q91286 mus musc
4	1410.5	64.0	542	13	Q90V66 Oryzob squallus aca
5	1243	56.4	250	6	Q95J30 Oryzob caris fami
6	1241.5	56.4	592	13	Q90W59 Oryzob baculatio
7	1216.5	56.1	553	13	Q90W59 Oryzob baculatio
8	1214.5	56.0	553	13	Q90W59 Oryzob baculatio
9	1220	55.4	565	13	Q90W59 Oryzob baculatio
10	1170.5	53.1	587	13	Q90W59 Oryzob baculatio
11	1065	48.3	587	13	Q90W59 Oryzob baculatio
12	1064	48.3	581	13	Q90W59 Oryzob baculatio
13	1053	47.8	569	13	Q90W59 Oryzob baculatio
14	1046.5	47.5	564	13	Q90W59 Oryzob baculatio
15	1021.5	46.4	441	6	Q90W59 Oryzob baculatio
16	1017	46.2	578	13	Q90W59 Oryzob baculatio

17	1004.5	45.6	620	13	Q90W59 Oryzob baculatio
18	985.5	44.7	554	13	Q90W59 Oryzob baculatio
19	961.5	43.6	491	13	Q90W59 Oryzob baculatio
20	949	43.1	391	13	Q90W59 Oryzob baculatio
21	942.5	42.8	335	13	Q90W59 Oryzob baculatio
22	942.5	42.8	276	13	Q90W59 Oryzob baculatio
23	942.5	42.8	200	13	Q90W59 Oryzob baculatio
24	925	42.8	101	12	Q923V1 Oryzob baculatio
25	912	42.8	484	5	Q90W59 Oryzob baculatio
26	912	42.8	406	6	Q90W59 Oryzob baculatio
27	906	42.8	249	6	Q90W59 Oryzob baculatio
28	901.5	42.8	710	13	Q90W59 Oryzob baculatio
29	876	42.8	583	13	Q90W59 Oryzob baculatio
30	868.5	42.8	753	13	Q90W59 Oryzob baculatio
31	860.5	42.8	438	13	Q90W59 Oryzob baculatio
32	858	42.8	939	6	Q90W59 Oryzob baculatio
33	857.5	42.8	689	13	Q90W59 Oryzob baculatio
34	857.5	42.8	732	13	Q90W59 Oryzob baculatio
35	848	42.8	790	13	Q90W59 Oryzob baculatio
36	842	42.8	87	6	Q90W59 Oryzob baculatio
37	842	42.8	155	13	Q90W59 Oryzob baculatio
38	841.5	42.8	401	13	Q90W59 Oryzob baculatio
39	840.5	42.8	360	13	Q90W59 Oryzob baculatio
40	837	42.8	688	13	Q90W59 Oryzob baculatio
41	834	42.8	906	4	Q90W59 Oryzob baculatio
42	834	42.8	982	6	Q90W59 Oryzob baculatio
43	833	42.8	848	13	Q90W59 Oryzob baculatio
44	833	42.8	87	6	Q90W59 Oryzob baculatio
45	831.5	42.8	740	4	Q90W59 Oryzob baculatio
46	830.5	42.8	895	6	Q90W59 Oryzob baculatio
47	830	42.8	793	11	Q90W59 Oryzob baculatio
48	830	42.8	794	11	Q90W59 Oryzob baculatio
49	830	42.8	866	6	Q90W59 Oryzob baculatio
50	829.5	42.8	853	13	Q90W59 Oryzob baculatio
51	826	42.8	763	13	Q90W59 Oryzob baculatio
52	825	42.8	854	13	Q90W59 Oryzob baculatio
53	824	42.8	692	13	Q90W59 Oryzob baculatio
54	821.5	42.8	732	4	Q90W59 Oryzob baculatio
55	821.5	42.8	769	13	Q90W59 Oryzob baculatio
56	821	42.8	839	13	Q90W59 Oryzob baculatio
57	817.5	42.8	525	6	Q90W59 Oryzob baculatio
58	817	42.8	563	13	Q90W59 Oryzob baculatio
59	816.5	42.8	346	4	Q90W59 Oryzob baculatio
60	814.5	42.8	340	5	Q90W59 Oryzob baculatio
61	813.5	42.8	436	5	Q90W59 Oryzob baculatio
62	811.5	42.8	303	4	Q90W59 Oryzob baculatio
63	811.5	42.8	414	11	Q90W59 Oryzob baculatio
64	809.5	42.8	400	13	Q90W59 Oryzob baculatio
65	804.5	42.8	797	13	Q90W59 Oryzob baculatio
66	804	42.8	414	5	Q90W59 Oryzob baculatio
67	803	42.8	763	13	Q90W59 Oryzob baculatio
68	802.5	42.8	363	5	Q90W59 Oryzob baculatio
69	801	42.8	444	13	Q90W59 Oryzob baculatio
70	799.5	42.8	448	5	Q90W59 Oryzob baculatio
71	799	42.8	322	11	Q90W59 Oryzob baculatio
72	792	42.8	412	13	Q90W59 Oryzob baculatio
73	791.5	42.8	475	5	Q90W59 Oryzob baculatio
74	789.5	42.8	159	6	Q90W59 Oryzob baculatio
75	787.5	42.8	427	5	Q90W59 Oryzob baculatio
76	787.5	42.8	448	13	Q90W59 Oryzob baculatio
77	781	42.8	127	6	Q90W59 Oryzob baculatio
78	780	42.8	379	13	Q90W59 Oryzob baculatio
79	776	42.8	422	13	Q90W59 Oryzob baculatio
80	774	42.8	643	6	Q90W59 Oryzob baculatio
81	773.5	42.8	427	13	Q90W59 Oryzob baculatio
82	773	42.8	422	13	Q90W59 Oryzob baculatio
83	771.5	42.8	424	6	Q90W59 Oryzob baculatio
84	771	42.8	348	13	Q90W59 Oryzob baculatio
85	770.5	42.8	467	5	Q90W59 Oryzob baculatio
86	770	42.8	480	5	Q90W59 Oryzob baculatio
87	770	42.8	489	5	Q90W59 Oryzob baculatio
88	767.5	42.8	609	13	Q90W59 Oryzob baculatio
89	766.5	42.8	232	13	Q90W59 Oryzob baculatio

90	464	16.5	408	1	Q9NCE1	Q9NCE1, keratin 19, non
91	459	16.3	549	11	Q9P6M1	Q9P6M1, rat tms not
92	459	16.3	560	11	Q9P6M1	Q9P6M1, rat tms not
93	459	16.3	627	11	Q9GZB6	Q9GZB6, mus mtrc11.1
94	438	16.3	545	4	Q16413	Q16413, hmo sapien
95	455.5	16.1	434	5	P917B0	P917B0, polyandro
96	455	16.1	456	11	Q9L119	Q9L119, tmmus sib
97	455	16.1	459	5	Q9G3C7	Q9G3C7, adcs aeryp
98	455	16.1	484	5	Q9G3C8	Q9G3C8, adcs aeryp
99	454.5	16.1	262	4	Q9H072	Q9H072, hmo sapien
100	454	16.1	594	5	Q9G041	Q9G041, hmo sapien
101	455.5	16.0	125	6	Q19009	Q19009, conus cabal
102	450	15.9	538	5	Q77100	Q77100, adcs aeryp
103	450	15.9	565	5	Q77099	Q77099, adcs aeryp
104	449	15.8	481	5	Q26641	Q26641, stronylce
105	448.5	15.8	485	4	Q9H4Y3	Q9H4Y3, adcs aeryp
106	447	15.8	541	4	Q9H070	Q9H070, hmo sapien
107	444	15.6	404	4	Q9H0B8	Q9H0B8, hmo sapien
108	443.5	15.6	448	13	Q9Z019	Q9Z019, hmo sapien
109	443	15.6	435	5	Q9G562	Q9G562, rtpodusa
110	442	15.5	445	11	Q9H341	Q9H341, mus musc
111	441.5	15.5	427	6	Q9TFF0	Q9TFF0, bos taurus
112	441.5	15.5	462	11	P97513	P97513, mus spracu
113	440.5	15.5	731	5	Q9H630	Q9H630, scistosoma
114	440	15.4	422	13	Q9H430	Q9H430, brachydan
115	439.5	15.4	448	13	Q9H065	Q9H065, brachydan
116	439	15.4	495	6	Q9G8K1	Q9G8K1, equus cabal
117	438	15.3	411	1	Q9H745	Q9H745, xenopus lae
118	438	15.3	517	13	Q9G416	Q9G416, brachydan
119	437.5	15.3	516	13	Q421B6	Q421B6, brachydan
120	436.5	15.3	284	13	Q9G0Y0	Q9G0Y0, put. cynom

A1.1 (NM;N)S

	RESULT 1
09EMED	PRELIMINARY:
09MEMO	PG# 459 AA.
01 DEC-2001 (TEMPREL: 19, Created)	
01 DEC-2001 (TEMPREL: 19, Last sequence update)	
01 JUN-2002 (TEMPREL: 21, Last annotation update)	
DEB ESTROGEN RECEPTOR beta Z.	
CN EMBETAZ.	
OS Mucosa associated (Stump failed mapping).	
EC EkkaYorai; Megazon; Chondral; Vertebral; Endocostal;	
ac Membrane; Embryonic; Primaries; Catarrhal; Corneothelial;	
cc Corneothelial; Maraca.	
OX NBT Takid 9640;	
RN [1]	
SEQUENCE FROM N.A.	
KA Schibye O.A., Wilson J.A., Mullar M.K., Macpherson S., Saunders P.T.;	
RT "The estrogen receptor beta variant ERbeta.c8/ERbeta.2 is expressed in	
RI a wide range of tissues in both old and New world primates."	
RL Submitted (JUN 2001) to the EMBL/Genbank/Joint databases	
CT 1 SIMILARITY LOCATION: NUCLEA (BY SIMILARITY).	
CC 1 SIMILARITY RELATIONS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.	
FEHML AC796165; AAK714711.	
DR InterPro: IPromis46; Hormone_rec_14.	
DR InterPro: IPromis428; Zinc_cysteinol_d.	
DR Pfam: PF00104; Hormone_rec_1.	
DR Pfam: PF00105; Z1_C4_1.	
DR Pfam: PF00039; Zinc_cysteine_d_1.	
DR PROSITE: PS00041; NUCLEAR RECEPTOR; UNKN_WN_1.	
KW DNA binding; Nuclear protein; Receptor; Transcription regulation;	
Zinc finger; Thiolase.	
SEQUENCE 499 AA: 557b2 MW: 491345Da pI:6.0A cMO64;	

Query Match	97.28;	Score 2141;	108 6;	Length 490;
Fast Local Similarity	96.98;	Prod. No. 6.2e-194;		
Matches 403;	Conserved Ivs	4;	Mismatches	9;
			Indels	0;
			Gaps	0;

07	1	MNSSTNSVNI	ELGSGROVTT	STNNV	WET	EGH	SH	VYHRE	SH	YAE	OK	SW	FAAS	60
1b	54	MNSSTNSVNI	ELGSGROVTT	STNNV	WET	EGH	SH	VYHRE	SH	YAE	OK	SW	FAAS	11
07	61	EHLFVRELL	EKESVGNIO	ASVPG	IGOSKE	PAHIO	AV	SVYAS	YAE	GVNS	EG	KAF	120	
1b	114	EHLFVRELL	EKESVGNIO	ASVPG	IGOSKE	PAHIO	AV	SVYAS	YAE	GVNS	EG	KAF	17	
07	121	KESLOHNDY	ETATMO	TTOR	NRKSK	VA	AK	RO	YEV	MYK	OS	REK	180	
1b	174	KESLOHNDY	ETATMO	TTOR	NRKSK	VA	AK	RO	YEV	MYK	OS	REK	234	
07	181	SABOR	H	AK	RK	RS	TH	PA	RVRELL	LA	LS	BO	VI	241
1b	234	SABOR	H	AK	RK	RS	TH	PA	RVRELL	LA	LS	BO	VI	29
07	241	MMSST	EL	AK	EL	VE	MI	SWAK	1	ET	VE	LS	ST	300
1b	294	MMSST	EL	AK	EL	VE	MI	SWAK	1	ET	VE	LS	ST	35
07	401	ETATMO	TTOR	NRKSK	VA	AK	RO	YEV	MYK	OS	REK	1	20	406
1b	454	ETATMO	TTOR	NRKSK	VA	AK	RO	YEV	MYK	OS	REK	1	20	461
07	461	VIA	LO	PA	D	SS	RR	KA	MI	NA	V	PA	LA	416
1b	414	VIA	LO	PA	D	SS	RR	KA	MI	NA	V	PA	LA	419

2

ID	Q55M99	PRELIMINARY?	PROT	486 AA
10	Q55M99			
11	01-DISE-2001 (TEMPEROL_19, created)			
12	01-DISE-2001 (TEMPEROL_19, last sequence update)			
13	01-JUN-2002 (TEMPEROL_21, last annotation update)			
14	ESTROGEN RECEPTOR BETA 2.			
15	EREB1A2.			
16	CELLULAR JACTAZIN (Common marmoset).			
17	FOKRYOLIN.			
18	Mammalia: Eutheria: Primates: Platyrrhini: Callitrichidae: Callithrix			
19	MB1_taxid=9483.			
20	[1]			
21	SEQUENCE FROM N.A.			
22	SCHEIDT G.A., WILLSON J.A., MILLER M.R., MACPHERSON S., SAUNDERS P.T.:			
23	"The estrogen receptor beta variant ESRB2-27962A2 is expressed in			
24	a wide range of tissues in both old and New World primates."			
25	Submitted (JUN-2001) via the EMBL/GenBank/JGI/DBI databases.			
26	1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
27	2. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.			
28	EMBL: AF34816; AAK7148.1;			
29	10101010; F06000546; HormoneRec_19.			
30	10101010; F06005428; Znf_454steroid.			
31	10101010; HormoneRec_1.			
32	10101010; Znf_44_1.			
33	10101010; Znf_454steroid.1.			
34	PROSITE: PS00043; NUCLEAR RECEPTOR, UNKNOWN 1.			
35	2.0.10101010; Nuclear protein; Receptor; Transcription regulation;			
36	Zinc finger			
37	SEQUENCE: 486 AA; 5454 MW; 4B2946507471E277 CRC64;			

[illegible]


```

DB InterPro: IPR000536: Hormone_rec_114
DB InterPro: IPR001292: Oestrdn_receptor
DB InterPro: IPR001723: Stdrnm_receptor
DB InterPro: IPR001628: Zn1_Castetoid
DB Pfam: PF00104: hormone_rec_1
DB Pfam: PF02159: oest_recpt_1
DB Pfam: PF00105: z1-c4_1
DB PRINTS: PR00398: STROBOMONER
DB PRINTS: PR00047: STROBOMONER
DB PROSITE: PS00045: Zn1_Castetoid_1
DB SMART: SM00430: H011_1
DB SMART: SM00399: Z0F_C4_1
DB PROSITE: PS00041: NUCLEAR_RECEPTOR; UNKNOWN_1
DB RECEPTOR
DB SOURCE: 587 AA; 66514 MW; DE17E2H847P0513 CRO64

Query Match 48.38; Score 1065; DB 13; Length 587;
Best Local Similarity 52.78; Pred. No. 4,4e+92;
Matches 214; Conservative 69; Mismatches 104; Indels 24; Gaps 8.

DB 22 SPVAVIQTPEHLSPIVVR-QLSHYAFPOKSPW--GTASSI FIELPVPETI KPVSSN 74
DB 100 SPVAVIQTPEHLSPIVVR-QLSHYAFPOKSPW--GTASSI FIELPVPETI KPVSSN 156
DB 79 PCASPVTPG---SKPDAPAVSTVAGVYHVTWSTPTVAFKPKKRS LQNDNYTCAI 135
DB 157 EPPASTSPVANSIMSTFETFTVAVTGVASGVYHVTWSTPTVAFKPKKRS LQNDNYTCAI 215
DB 134 ATNCTITDKNRKRSQATFETNCTVGVANVNSPEPPTVGLVPLVPSATGCTGVAAG 194
DB 217 ATNCTITDKNRKRSQATFETNCTVGVANVNSPEPPTVGLVPLVPSATGCTGVAAG 274
DB 194 KSGNHAPV--RELIID-----ALSPQIVLTLLEPPHILIS-PPSAPFTASM 241
DB 277 TAPPTTITWTSNVLFTKPKNSPA-STAPDMSALFAPPTVAVTTPHTNAPM 248
DB 242 MMSITKADKETVHMTSMARKTPGEVLSLPLVPLIFSGVMEVLMNIMMSITKAPRI 301
DB 437 MLTINLADELIVHMLNMAKPVGVFLDTHLVVHIFPAWFLIMMIVMSVSSGAG 396
DB 462 TPATLVTSNDRKCVYVHIFPMATLSPP-PLTGVKGVVAVNGLNLSMAGV 431
DB 497 LFAVNLIDNDRKCVYVHIFPMATLSPP-PLTGVKGVVAVNGLNLSMAGV 514
DB 462 LADVDASPKLAL-ELINAVTALVWVAVGVTSQVSGMPLANIMLSHVR 414
DB 457 SSTKSLKEGVHRAVTKITPTTTHVAKSGLSLQGHRAVGLIITLSIRK 510

RESULT 12
DB 098SM9 PRELIMINARY: PRT: 581 AA.
DB 01-MAR-2002 (TREMBlrel. 20, Created)
DB 01-JUN-2002 (TREMBlrel. 20, Last sequence update)
DB 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DB Estragen receptor.
DB ER.
DB Chromidophorus unipareus (Whiptail lizard)
DB Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
DB Lepidodactylia: Squamata: ScleroGLOSSA: Scincomorpha: Teiioidea:
DB Teiioidea: Chromidophorus.
DB NCBI_TaxID: 47197;
DB KN SEQUENCE FROM N.A.
DB RX MENLNF 2143727; F.A.Med 1164222;
DB KA Sumida K., Oke N., Saito K., Kaneko H.;
DB "Molecular cloning and characterization of reptilian estrogen receptor
DB cDNAs."
DB Mol. Cell. Endocrinol. 181:31-39(2001).
DB EMBL: AB05221; BAB79437.1;
DB InterPro: IPR000536: Hormone_rec_114
DB InterPro: IPR001292: Oestrdn_receptor
DB InterPro: IPR001723: Stdrnm_receptor

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DB InterPro: IPR001723: Stdrnm_receptor
DB InterPro: IPR001628: Zn1_Castetoid
DB Pfam: PF00104: hormone_rec_1
DB Pfam: PF02159: oest_recpt_1
DB Pfam: PF00105: z1-c4_1
DB PRINTS: PR00398: STROBOMONER
DB PRINTS: PR00047: STROBOMONER
DB PROSITE: PS00045: Zn1_Castetoid_1
DB SMART: SM00430: H011_1
DB SMART: SM00399: Z0F_C4_1
DB PROSITE: PS00041: NUCLEAR_RECEPTOR; UNKNOWN_1
DB RECEPTOR
DB SOURCE: 581 AA; 66560 MW; A9916C44P03058 CRO64

Query Match 48.38; Score 1064; DB 13; Length 581;
Best Local Similarity 51.08; Pred. No. 5,4e+92;
Matches 214; Conservative 71; Mismatches 95; Indels 40; Gaps 8.

DB 22 SPVAVIQTPEHLSPIVVR-QLSHYAFPOKSPW--GTASSI FIELPVPETI KPVSSN 74
DB 100 SPVAVIQTPEHLSPIVVR-QLSHYAFPOKSPW--GTASSI FIELPVPETI KPVSSN 156
DB 79 PCASPVTPG---SKPDAPAVSTVAGVYHVTWSTPTVAFKPKKRS LQNDNYTCAI 135
DB 157 EPPASTSPVANSIMSTFETFTVAVTGVASGVYHVTWSTPTVAFKPKKRS LQNDNYTCAI 215
DB 134 ATNCTITDKNRKRSQATFETNCTVGVANVNSPEPPTVGLVPLVPSATGCTGVAAG 194
DB 217 ATNCTITDKNRKRSQATFETNCTVGVANVNSPEPPTVGLVPLVPSATGCTGVAAG 274
DB 194 KSGNHAPV--RELIID-----ALSPQIVLTLLEPPHILIS-PPSAPFTASM 241
DB 277 TAPPTTITWTSNVLFTKPKNSPA-STAPDMSALFAPPTVAVTTPHTNAPM 248
DB 242 MMSITKADKETVHMTSMARKTPGEVLSLPLVPLIFSGVMEVLMNIMMSITKAPRI 301
DB 437 MLTINLADELIVHMLNMAKPVGVFLDTHLVVHIFPAWFLIMMIVMSVSSGAG 396
DB 462 TPATLVTSNDRKCVYVHIFPMATLSPP-PLTGVKGVVAVNGLNLSMAGV 431
DB 497 LFAVNLIDNDRKCVYVHIFPMATLSPP-PLTGVKGVVAVNGLNLSMAGV 514
DB 462 LADVDASPKLAL-ELINAVTALVWVAVGVTSQVSGMPLANIMLSHVR 414
DB 457 SSTKSLKEGVHRAVTKITPTTTHVAKSGLSLQGHRAVGLIITLSIRK 510

RESULT 13
DB 098SM9 PRELIMINARY: PRT: 569 AA.
DB 01-JUN-2001 (TREMBlrel. 17, Created)
DB 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DB 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DB Estragen receptor alpha.
DB Brachydactylus teio (zebra danio).
DB Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
DB Actinopterygii: Neopterygii: Teleostei: Ostariophysi: Cypriniformes:
DB Cyprinidae: Danio.
DB NCBI_TaxID: 7955;
DB KN SEQUENCE FROM N.A.
DB RP TISSUE: LIVER;
DB KA Akita H., Kishida M., Callard G.V.;
DB "Estrogen receptor cDNAs in zebrafish."
DB Mol. Cell. Endocrinol. 181:31-39(2001).
DB "1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)."
DB EMBL: AF349412; AAK16740.1;
DB HSSP: P03472; IICP.
DB InterPro: IPR000536: Hormone_rec_114
DB InterPro: IPR001292: Oestrdn_receptor
DB InterPro: IPR001723: Stdrnm_receptor

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[illegible][illegible]

10b 508 LRRGVASSUREYQTLKIM 527

RESULT 40

ID Q90ZM7 PRELIMINARY: PRT: 704 AA.

AC Q90ZM7/

01-JUN-2002 (TEEMUREL: 20, created)

01-MAR-2002 (TEEMUREL: 20, last sequence update)

01-JUN-2002 (TEEMUREL: 21, last annotation update)

DE Vertebrate receptor (transmembrane)

OS Xenopus laevis (African clawed frog)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;

OC Xenopus; Xenopus

OC NCBI_TaxID: 8559

OX [1]

SEQUENCE FROM N.A.

RA Tian J., Ruderman J.V.:

RT "Cloning of a progesterone receptor MPR-2 from Xenopus laevis

RT cDNA"

KL Submitted (MAY 2000) to the EMBL/Genbank/CCPC databases.

DE EMBL: AF195966; AN:55260; J:

DE DefectPro: IP6000546; hormone_rec_119.

DE DefectPro: IP6000128; Progesterone_receptor.

DE DefectPro: IP6001743; Steroid_receptor.

DE DefectPro: IP6001628; zn1_casteroid.

DE DefectPro: IP600104; hormone_rec_1.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

RESULT 41

ID Q90ZM7 PRELIMINARY: PRT: 438 AA.

AC Q90ZM7/

01-JUN-2001 (TEEMUREL: 19, created)

01-MAR-2001 (TEEMUREL: 19, last sequence update)

01-JUN-2002 (TEEMUREL: 21, last annotation update)

DE Vertebrate receptor (transmembrane)

OS Xenopus laevis (African clawed frog)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Hypselostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;

OC Xenopus; Xenopus

OC NCBI_TaxID: 8559

OX [1]

SEQUENCE FROM N.A.

RA Tian J., Ruderman J.V.:

RT "Cloning of a progesterone receptor MPR-2 from Xenopus laevis

RT cDNA"

KL Submitted (MAY 2000) to the EMBL/Genbank/CCPC databases.

DE EMBL: AF195966; AN:55260; J:

DE DefectPro: IP6000546; hormone_rec_119.

DE DefectPro: IP6000128; Progesterone_receptor.

DE DefectPro: IP6001743; Steroid_receptor.

DE DefectPro: IP6001628; zn1_casteroid.

DE DefectPro: IP600104; hormone_rec_1.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

DE DefectPro: IP600105; zn1_casteroid.

01-JUN-2002 (TREMblrel. 21, last annotated update)
 DE Progesterone receptor.
 GN PR.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Lanthier-van Leuven I S., van Garderen E., Mol J.A.;
 RT "Molecular cloning and cellular localization of the canine
 progesterone receptor."
 RL Submitted (AUG-1999) to the EMBL/Genbank/DDBJ databases
 CC -1- SUPPLEMENTARY LOCATIONS: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DR EMBL: AF177470; AAG09282.1; -
 DR HSSP: P06401; 1A28;
 DR InterPro: IPRO00346; Hormone_Recep_1;
 DR InterPro: IPRO01283; Progesterone_Receptor;
 DR InterPro: IPRO01723; Steroid_Receptor;
 DR InterPro: IPRO01628; Zinc_Catalyst;
 DR Pfam: PF00104; hormone_rec_1;
 DR Pfam: PF02161; Prog.Receptor; 1;
 DR Pfam: PF01165; Z-C4; 1;
 DR PRINTS: PR00398; STERHORMER.
 DR PROSITE: PS00477; STER-RECEPT.
 DR ProDom: PD000035; Zinc_Catalyst; 1;
 DR SMART: SM00399; ZNF_C4; 1;
 DR SMART: SM00399; ZNF_C4; 1;
 DR PROSITE: PS00011; NUCLEAR_RECEPTOR; 1;
 DR DNA-binding: Nuclear Protein Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE 939 AA: 98417 MW: 14485356A6F239 C9C64;
 Query Match 20.8%; Score 458; DB 6; Length 939;
 Best Local Similarity 32.5%; Prod No 26-74;
 Matches 106; Conservative 64; Mismatches 126; Indels 40; Gaps 10;
 QY 96 CAVSTVASYAVHGVWSTVEGCKAFKRSLSQHNINYPATNCTTDKPKRSCQACPLK 155
 DB 573 CILCGFASCHRYVATLFGSTVFTRKAFKRGHNITVAPNITVTKIPKNTACTGPK 632
 QY 156 CEEGVNKGKSPREKQVPLVPRQPSAEQD--HCAKAKPSGSHAPVAPKLLIALSPK 213
 DB 633 CCGACNVLAGPKFK--FNKRVPMPTLDAVALPQVGIIPNESQALSGIT-----SEPS 684
 QY 214 Q-----LVTLLEPRPHVILSRSA-PTEAEMMSSTKLADKELVIMISWAKKIPG 265
 DB 685 QDILPLPLINLMSLIPVIVYAGHNITKPIPTSSSLISLNDJDEQDLSSVKKSKSLPG 744
 QY 266 PVEISTPQVPLESWMFVLMKIMWSTSTHFG--KLIFAVLVDPKPKVWGHIF 323
 DB 745 FRLIATIDQITLIGVSMWSTVGRGWSYKRVASQIMYPADILNLNPKK--PSSEPS 803
 QY 424 FFMILATTSPPPELKTQKEVYLVKAMILLNSMTGVTATVPAISPPYLAHLIAVITA 483
 DB 804 CLTMMQIPQGFVKIYVSGPEFLVMYVITLINT--PL-----PGLPSQWLFEMSSYLE 857
 QY 384 LVMVIA--KSGISSQOOSMLANLL 406
 DB 858 LTKATGLRQKGVVSSQSPFYHILTKIM 883
 RESULT 33
 Q98GX5 PRELIMINARY: PRT: 689 AA.
 ID Q98GX5
 AC Q98GX5
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Progesterone receptor type 2
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Anguilla japonica. Telostei. Anguilliformes. Anguillidae;
 OC Anguilla.
 GN NCBI_TaxID=7937;
 RN (1)
 RP SEQUENCE FROM N.A.
 RT TISSUE=TESTIS;
 KX MEDLINE=21629085; PubMed=1175535;
 RA Ikeuchi T., Todo T., Kobayashi T., Nagahama Y.;
 RT "A novel progesterone receptor subtype in the Japanese eel, Anguilla
 japonica."
 EL FEBS Lett. 510:77 82(2002).
 DR EMBL: AB028024; BAB85993.1; -
 KW Receptor
 SQ SEQUENCE 689 AA: 76316 MW: F0BDB5AC7A72AC C9C64;
 Query Match 20.8%; Score 457.5; DB 13; Length 689;
 Best Local Similarity 30.3%; Prod No. 156-34;
 Matches 118; Conservative 72; Mismatches 157; Indels 43; Gaps 12;
 QY 41 QSHLYAEPPQKSPWCEAPSELETLIPVNPETLKPKVSCNPA-----SPVTSPSSKP 92
 DB 263 KSLPTSPSSQSWDSTGLSEDFEETGYLPGLPPICTHNSLKSRYVMGMISQK- 321
 QY 93 AHPQAVCSYASYHGVWSTVEGCKAFKRSLSQHNINYPATNCTTDKPKRSCQACPLK 152
 DB 422 --FLLIDSEASCHYGVITQSSCKVFKKAVRGHNITVAPNITVTKIPKNTACTGPK 379
 QY 153 IPKQEVNKGKSPREKQVPLVPRQPSAEQD--YIPVPPQSPAPQHPVAPVSHAPV 203
 DB 380 LPRQVAGVMTIGPKPKKLALKVLGLDQSLAVSPGLASYP-----SCALALISPKMVR 435
 QY 204 ELLDLSPDLVTLLEPRPHVILSRSA--PTESAMMSSTKLADKELVIMISWAK 261
 DB 436 EL---QFTQ--ILSTLEIPETVSYSDATQPEPTELLNSLGLFRLIMIVKSK 490
 QY 262 KIPQEVNKGKSPREKQVPLVPRQPSAEQD--YIPVPPQSPAPQHPVAPVSHAPV 319
 DB 491 SLGPFSLHINDQMTLIQYSMWSLWFSQWSPQNVREFYAPDLIDEEKMK----- 546
 QY 320 LLEHEMLLA--HSFELKIKKEVLYVAMILLNSMTGVTATVPAISPPYLAHLIAVITA 376
 DB 547 NSPTSLDMAMQIIPQAFINLQVYKEEFLQKQVLLILNT--VPLEGLSQADPQPKRGY 604
 QY 377 INAVTDAIWMVIAKSGISSQOOSMLANLL 406
 DB 605 IPFLTKA--IQITPEVMASSQPFYHILTKIM 633
 RESULT 34
 Q9DD09
 ID Q9DD09 PRELIMINARY: PRT: 732 AA
 AC Q9DD09
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE Progesterone receptor.
 GN XPR-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20570484; PubMed=11114187;
 RA Tian J., Kim S., Helling F., Ruderman J.V.;
 RT "Identification of XPR-1, a progesterone receptor required for Xenopus
 oocyte activation."
 RT Proc Natl Acad Sci U S A 97:14358-14364(2000).
 CC -1- SUPPLEMENTARY LOCATIONS: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DR EMBL: AF279335; AN042362.1; -
 DR HSSP: P06536; 1R6D.


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DE InterPro: IPR000546; Hormone_rec_119.
DE InterPro: IPR001248; Progester_receptor.
DE InterPro: IPR001248; Steroid_receptor.
DE InterPro: IPR001628; Znf_C4steroid.
DE Pfam: PF00104; hormone_rec_1.
DE Pfam: PF02161; prog_receptor_1.
DE Pfam: PF00105; zt_c4_1.
DE PROSITE: PS00098; Steroid_hormone.
DE PROSITE: PS00047; Steroid_hormone.
DE PROSITE: PF00005; Znf_C4steroid_1.
DE SMART: SM00430; Znf_C4_1.
DE SMART: SM00399; Znf_C4_1.
DE PROSITE: PS00041; Nuclear_receptor_1.
DE DNA-binding: Nuclear protein receptor; Transcription regulation.
KW Zinc finger.
SO SPOUNCE: 742 AA; 64022 MW; IPIR000414F022199 CR664.

Query Match: 20.8%; Score: 457.5; DB: 13; Length: 742;
Best Local Similarity: 40.2%; Prod. No. 1.6e-34;
Matches: 110; Conservative: 71; Mismatches: 120; Indels: 63; Gaps: 12;

DE 65 PVNFKETKKKVSNGRVSVPVPGSKRIAHFPAVGSVASCYHYGVMSCEGKAPKRSI 124
DE 654 PSEFETFPQKTI-----CLTGDASGTHGVLTGVSCKVFKKAI 193
DE 125 QSHNDYICPATNGCTIDKRRKRSVACRLKCYEWMVWCKSRRCGYRIVRKRSAD 184
DE 694 EYDHNICAGRNIGTVDKIRKKNICSLKRCQGVAGVCGKPKPG--RIKTRREID 451
DE 185 -----QLRARKAKR--SGHDPVPEPLIDALSPEDLVLTLFAEPPIVLS--P 231
DE 452 VLGSPPTLSLEFVQTLIRISNSSAQLD-----PPE--TLQITQSTPEVVAAYD 503
DE 242 PSATFEASMMSTIKLAKELVIDIMSMARKIDCEVELSLFQVALLSCMEVIMGLM 291
DE 504 NIDQETPSALISLNLCEKGLVYVKKSKSLGGRNLIHQDTLLQYSMMSLMVALG 563
DE 292 WRSTIDPG--KLFAHGLVLDGDK-----VEGILTFPMLLATTSPREKIDRK 342
DE 564 WRSGVGVSGMVFADLTINQKMKDSSEYTLIS---MMQIDQEFMKIQLVHE 615
DE 443 EYLVKAMILLNSMYPVATGADISKRKAHLINAVVIDMVAWLAKSGISSQGSRL 402
DE 615 ELPFMALLLNI ELPGLSKGLNIPKMSNYIPELAKA DLRKGVLAASQGVYL 672
DE 403 ANIL 406
DE 1
DE 673 TKLM 676

RESULT 45
P/00048 PRELIMINARY: PRT: 790 AA.
ID P/00048
AC P/00048
DE 01 FEB-1997 (Tremblat, 02, created)
DE 01 JUN 1999 (Tremblat, 09, last sequence update)
DE 01 JUN 2002 (Tremblat, 21, last annotation update)
DE Androgen receptor alpha isoform.
DE XL ALPHA AK.
DE Xenopus laevis (African clawed frog).
DE Eukaryotic Metazoa; Chordata; Vertebrata; Euteleostomi;
DE Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
DE Xenopodidae; Xenopus.
DE MPO ToxID 8655.
DE 11
DE SEQUENCE FROM N.A.
DE MEDLINE: 94376782; PubMed: 7690145;
DE Fischer L.M., Katz D., Kelley D.J.
DE "An androgen receptor mRNA isoform associated with hormone-induced
DE cell proliferation."
DE Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258(1993).
DE 121
DE SEQUENCE FROM N.A.

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DE MEDLINE: 95424753; PubMed: 7401402;
DE Fischer L.M., Katz D., Kelley D.B.
DE "Androgen-directed development of the Xenopus laevis gonad; control
DE of androgen receptor expression and tissue differentiation."
DE Dev. Biol. 170:115-126(1995).
DE 14
DE SEQUENCE FROM N.A.
DE Kelley D.B., Kamowitz E.R., Kelley D.B., Radu T.C.
DE Submitting (Apr 1998) to the EMBL/Genbank/Joint databases.
DE 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DE 1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DE EMBL: U67129; AAC97386.1.
DE HSP94: P06536; 1000.
DE InterPro: IPR001103; Androg_receptor.
DE InterPro: IPR000546; Hormone_rec_119.
DE InterPro: IPR001628; Znf_C4steroid.
DE Pfam: PF02166; Androgen_recep_1.
DE Pfam: PF00104; hormone_rec_1.
DE Pfam: PF00105; zt_c4_1.
DE PROSITE: PS00047; Steroid_hormone.
DE PROSITE: PF00005; Znf_C4steroid_1.
DE SMART: SM00430; Znf_C4_1.
DE SMART: SM00399; Znf_C4_1.
DE PROSITE: PS00041; Nuclear_receptor_1.
DE DNA-binding: Nuclear protein receptor; Transcription regulation.
KW Zinc finger.
SO SPOUNCE: 790 AA; 86973 MW; 9E7EC136CC3906 CR664.

Query Match: 20.3%; Score: 448; DB: 13; Length: 790;
Best Local Similarity: 28.6%; Prod. No. 1.4e-33;
Matches: 125; Conservative: 73; Mismatches: 151; Indels: 88; Gaps: 15;

DE 3 YSTPSNVTLEGGPGKQUTSPNVMLTPGHLSPVYVHQVLSHLYAEYK--SPWCPA-- 57
DE 353 YSYPRG---HGVADAEPEPSDW---YPAITGVH---PYSQPKTGMAMMREYD 401
DE 58 -----KLEHTLPVKKETLKKKVSNGKASVITPGSKRIAHF-----CAVSIYA 103
DE 402 GAFEMRLKEGGRIHLP-----DYEPQKTCITLGDIA 446
DE 104 SGYHYGVMSCEGKAPKRSIQSHNDYICPATNGCTIDKRRKRSVACRLKCYEWMV 163
DE 447 SGYHYGVMSCEGKAPKRSIQSHNDYICPATNGCTIDKRRKRSVACRLKCYEWMV 495
DE 164 GSRREKCYRLVPRKRSADQLHCAKAKRSAGH--APVRELLIDALSPEDLVLTL 220
DE 496 -----LAPKIKKIGNKAGPEIPSSVAGPEPSKPI SPDMGIDQLPYSVQPIPNV 548
DE 221 EAPPIVLS--PSATFEASMMSTIKLAKELVIDIMSMARKIDCEVELSLFQVALL 278
DE 549 EATPEVAVVAGHNNQDPSFALLSLNLELGRVLIYVKKKAKALPGRKILVSGMVI 608
DE 609 QVSMGLIMFAMVMSKRVNSRMIVFADLVFNRYRMKRSMSQVVR-----LRH 660
DE 440 TTSKPEELKQIKREYGVVAMILLNSMYPVATGADISKRKAHLINAVVIDMVA 489
DE 661 LSGPGLQIPEELAKALLF--SLP--VEGLKDKCTEDEMNTIKELGVLSKR 717
DE 490 KSLSSSQGSRLANIL 406
DE 718 NIFASSRKPEFOLTKIL 734

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AC G9N0K2
DE 01-067-2000 (Tremblat, 15, created)
DE 01-067-2000 (Tremblat, 15, last sequence update)
DE 01-JUN-2002 (Tremblat, 21, last annotation update)
DE Estradiol receptor beta (Fragment).

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08 E-RECEPTOR SUS
 09 Sus scrofa (pig)
 00 Eukaryota: Metazoa: Chordata: Canidae: Vertebrata: Eumetazoa
 01 Mammalia: Eutheria: Cetartiodactyla: Suidae: Sus
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RESULT 37

Q90023

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DT

01-MAR-2001 (TRENKREL 16, Created)

DT

01-JUN-2002 (TRENKREL 21, Last sequence update)

DE

Estrogen receptor subtype II (Flaumen)

OS

Microperis salmoides (Largemouth bass)

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

AC

Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei:

OC

Acanthopterygii: Acanthopterygii: Perciformes: Percoidae:

OC

Centrarchidae: Microperis:

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OM nucleotide search, using SW model

Run on: June 16, 2003, 00:23:52 ; Search time 3329.11 seconds

(without alignments)
10988 581 Million cell updates/sec

Title: US-08-826-361A-20

Perfect score: 1257

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Scoring table:

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

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21	1127	89.7	1566	9	AF394816	AF394816 Callithrix
22	1125	89.5	1651	9	AF177936	AF177936 C. jacchus m
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24	987	78.5	1611	4	AF110402	AF110402 Bos tauru
25	985	78.4	1820	4	AF164957	AF164957 Sus scrofa
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51	654	52.1	1558	10	AF042061	AF042061 Rattus no
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53	554	44.1	3061	5	AB003456	AB003456 Anouilla
54	439	35.0	716	4	AF252109	AF252109 Ovis arie
55	426	33.9	1937	5	AF144567	AF144567 Dario rot
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57	423	33.7	2850	5	AB070630	AB070630 Paratichl
58	413	32.9	2284	5	AT061269	AT061269 Carassius
59	403	32.1	1909	5	AB083064	AB083064 Cyprinus
60	403	32.0	2276	5	AB070901	AB070901 Cyprinus
61	402	31.4	4306	5	IN075605	IN075605 Tilapia nil
62	394	31.4	2508	5	CMY28988	CMY28988 Cyprinus
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 VERSION AX323055.1 GI:18094942
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 Moselman, S. and Dijkema, R.
 AUTHOR TITLE Chimeric hormone receptor
 JOURNAL Patent: EP 1162264 A 1 12-DEC 2001.
 AKZO Nobel N.V. (NL)
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 DEFINITION Sequence 4 from Patent W9709348.
 ACCESSION A61586
 VERSION A61586.1 GI:3715917
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 1460)
 AUTHOR Kujner G.G., Emark, E. and Gustafsson, J.
 TITLE ORPHAN RECEPTOR
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DB 747 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
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DB 807 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 841 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 867 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 901 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 927 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 961 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 987 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1021 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1047 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1081 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1107 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1141 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1167 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1201 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1227 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

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DEFINITION Sequence 4 from Patent EP0935000.
ACCESSION AX022458
VERSION AX022458.1 GI:10046069
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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BASE COUNT 452 a 479 c 411 g 418 t
Query Match 99.28; Score 1247; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1,66-271;
Matches 1247; conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 327 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 361 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 387 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
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UY 601 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 627 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 661 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 687 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 721 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 747 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 781 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 807 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 841 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 867 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 901 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 927 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
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DB 987 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1021 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1047 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1081 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1107 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1141 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
DB 1167 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
UY 1201 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
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[illegible]

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DEFINITION	Sequence 24 from Patent EP162264.			
ACCESSION	AX323078			
VERSION	AX323078.1	G1:16093960		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			

[illegible]

JOURNAL

Submitted (03 Nov 1999) to: Scientific Medical Research Council,
Centre for Reproductive Biology, 47 Chalmers Street, Edinburgh, EH3
9PW, UK
on Nov 15, 1999. This sequence version replaced q1:1669661.

COMMENT

Related entries: X93101 & 057439.

FEATURES

SOURCE

Location/Qualifiers

1..1651

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BASE COUNT

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ORIGIN

Query Match

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Matches 1171; Conserved 0; Mismatches 76; Indels 0; Gaps 0;

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DB	331	ATGAAATACAGCTTCCGAGCAATCTGCTAACTTGTGAAGCGAGCTGTGTGGAGACG	390
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DB	991	ATGAAATACAGCTTCCGAGCAATCTGCTAACTTGTGAAGCGAGCTGTGTGGAGACG	1050
UY	841	ATGAAATACAGCTTCCGAGCAATCTGCTAACTTGTGAAGCGAGCTGTGTGGAGACG	900
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RESULT 23

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PubMed

REFERENCES

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TITLE

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RESULT 24
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DEFINITION
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AF110402
VERSION
AF110402.1 GI:4580595
KEYWORDS
Bos taurus.
SOURCE
Bos taurus.
ORGANISM
Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
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and Lubahn, D.B.
Cloning, sequencing, and localization of bovine estrogen
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JOURNAL
MEDLINE
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PUBMED
10926117
REFERENCE
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and Lubahn, D.B.
Direct Submission
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Campus Drive, Columbia, MO 65211, USA
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QY	121	CAGTATCAATCTGTATGGAGAACTTAAAGTGGCTGGTGGTCAAGCAGATGCTCTA	180	
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DB	397	GACATACCTTACCTTAAATATACATACATCAAAAGCAACTTATGATGATGAAAGCTGCT	456	
QY	241	CTCAAGCTGTACTGATGAGCTGAGCTTCAAAAGAGATGCTGATCTTGGCTGGCTGGCTGAG	300	
DB	457	CTCAAGCTGTACTGATGATGAGCTGAGCTTCAAAAGAGATGCTGATCTTGGCTGGCTGGCTGAG	516	
QY	301	GATTACGATCGGATATATATATGATGCTGGTGGTGGAGAGATGAAAGCTTTT	360	
DB	517	GATTATGCACTGGGATATATATATGATGCTGGTGGTGGAGAGATGAAAGCTTTT	576	
QY	361	AAAGAGAGCATTAACAT	420	
DB	577	AAAGAGAGCATTAACAT	636	
QY	421	GATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480	
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QY	481	ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540	
DB	697	ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	756	
QY	541	ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	600	
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QY	721	ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780	
DB	937	ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	996	
QY	781	AAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	840	
DB	997	AAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1056	
QY	841	GGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	900	
DB	1057	GGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1116	
QY	901	CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	960	
DB	1117	CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1176	
QY	961	CTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1020	
DB	1177	CTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1236	
QY	1021	CATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1080	

[illegible]

[illegible][illegible]

GenCore version 5.1.6
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OM nucleotide - nucleotide search, using SW model

Run on: June 15, 2003 23:19:19 ; Search time 298.206 Seconds

(without alignments)
98.22000 Million cell updates/sec

Library: US-08-826-361A-20

Perfect score: 1257

GenATPACAGCATTCACAT

Sequence: 1 ATGATTCACAGCATTCACAT

Scoring table:

IDENTITY: 100%

Gapop: 10.0 ; Gapext: 1.0

Search: 2185339 seqs 110000000 residues

Total number of hits satisfying chosen parameters: 4370470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Listing first 120 summaries

Databases:

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1: N_GenSeq_101002.*
2: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1960_PAT.*
3: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1961_PAT.*
4: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1962_PAT.*
5: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1963_PAT.*
6: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1964_PAT.*
7: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1965_PAT.*
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14: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1972_PAT.*
15: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1973_PAT.*
16: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1974_PAT.*
17: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1975_PAT.*
18: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1976_PAT.*
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21: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1979_PAT.*
22: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1980_PAT.*
23: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1981_PAT.*
24: /SITS2/qpdata/qgeneseq/qgeneseq-comb1/NA1982_PAT.*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	1257	100.0	1257	18	Human estrogen re
2	1257	100.0	1257	24	Human estrogen re
3	1249	99.4	1251	18	Human estrogen re
4	1249	99.4	1251	24	Human estrogen re
5	1247	99.2	1434	18	Human estrogen re
6	1247	99.2	1434	24	Human estrogen re
7	1247	99.2	1460	18	Human estrogen re
8	1247	99.2	1467	20	Human estrogen re
9	1247	99.2	1486	20	Human estrogen re

10	1247	99.2	1740	22	Human estrogen re
11	1247	99.2	1898	24	Human estrogen re
12	1247	99.2	1336	18	Human estrogen re
13	1247	99.2	1211	18	Human estrogen re
14	1247	99.2	2011	22	Human estrogen re
15	1247	99.2	2433	24	Human estrogen re
16	1247	99.2	1460	20	Human estrogen re
17	1247	99.2	1820	20	Human estrogen re
18	1247	99.2	1820	20	Human estrogen re
19	1247	99.2	1820	20	Human estrogen re
20	1247	99.2	1820	20	Human estrogen re
21	1247	99.2	1820	20	Human estrogen re
22	1247	99.2	1820	20	Human estrogen re
23	1247	99.2	1820	20	Human estrogen re
24	1247	99.2	1820	20	Human estrogen re
25	1247	99.2	1820	20	Human estrogen re
26	1247	99.2	1820	20	Human estrogen re
27	1247	99.2	1820	20	Human estrogen re
28	1247	99.2	1820	20	Human estrogen re
29	1247	99.2	1820	20	Human estrogen re
30	1247	99.2	1820	20	Human estrogen re
31	1247	99.2	1820	20	Human estrogen re
32	1247	99.2	1820	20	Human estrogen re
33	1247	99.2	1820	20	Human estrogen re
34	1247	99.2	1820	20	Human estrogen re
35	1247	99.2	1820	20	Human estrogen re
36	1247	99.2	1820	20	Human estrogen re
37	1247	99.2	1820	20	Human estrogen re
38	1247	99.2	1820	20	Human estrogen re
39	1247	99.2	1820	20	Human estrogen re
40	1247	99.2	1820	20	Human estrogen re
41	1247	99.2	1820	20	Human estrogen re
42	1247	99.2	1820	20	Human estrogen re
43	1247	99.2	1820	20	Human estrogen re
44	1247	99.2	1820	20	Human estrogen re
45	1247	99.2	1820	20	Human estrogen re
46	1247	99.2	1820	20	Human estrogen re
47	1247	99.2	1820	20	Human estrogen re
48	1247	99.2	1820	20	Human estrogen re
49	1247	99.2	1820	20	Human estrogen re
50	1247	99.2	1820	20	Human estrogen re
51	1247	99.2	1820	20	Human estrogen re
52	1247	99.2	1820	20	Human estrogen re
53	1247	99.2	1820	20	Human estrogen re
54	1247	99.2	1820	20	Human estrogen re
55	1247	99.2	1820	20	Human estrogen re
56	1247	99.2	1820	20	Human estrogen re
57	1247	99.2	1820	20	Human estrogen re
58	1247	99.2	1820	20	Human estrogen re
59	1247	99.2	1820	20	Human estrogen re
60	1247	99.2	1820	20	Human estrogen re
61	1247	99.2	1820	20	Human estrogen re
62	1247	99.2	1820	20	Human estrogen re
63	1247	99.2	1820	20	Human estrogen re
64	1247	99.2	1820	20	Human estrogen re
65	1247	99.2	1820	20	Human estrogen re
66	1247	99.2	1820	20	Human estrogen re
67	1247	99.2	1820	20	Human estrogen re
68	1247	99.2	1820	20	Human estrogen re
69	1247	99.2	1820	20	Human estrogen re
70	1247	99.2	1820	20	Human estrogen re
71	1247	99.2	1820	20	Human estrogen re
72	1247	99.2	1820	20	Human estrogen re
73	1247	99.2	1820	20	Human estrogen re
74	1247	99.2	1820	20	Human estrogen re
75	1247	99.2	1820	20	Human estrogen re
76	1247	99.2	1820	20	Human estrogen re
77	1247	99.2	1820	20	Human estrogen re
78	1247	99.2	1820	20	Human estrogen re
79	1247	99.2	1820	20	Human estrogen re
80	1247	99.2	1820	20	Human estrogen re
81	1247	99.2	1820	20	Human estrogen re
82	1247	99.2	1820	20	Human estrogen re

QY	78	AAATAATTCAGATCTTCTGAACTGAGCGCTCTACCAAAATGGCGCTCTGAGAA	841
DB	781	AAATAATTCAGATCTTCTGAACTGAGCGCTCTACCAAAATGGCGCTCTGAGAA	840
QY	841	TCCTGATGAGAGTGTATATCATATGAGCGCTGATGCGCTGCAATTCAGCGCGGTAAG	900
DB	841	TCCTGATGAGAGTGTATATCATATGAGCGCTGATGCGCTGCAATTCAGCGCGGTAAG	900
QY	901	GTATCTTGTGTGCAATCTCTGTCTGCAAGAAATGAGGCAAAATGCTATCAAGAAAT	960
DB	901	GTATCTTGTGTGCAATCTCTGTCTGCAAGAAATGAGGCAAAATGCTATCAAGAAAT	960
QY	961	GTGCAATTCCTGCAATCTCTGTCTGCAAGAAATGAGGCAAAATGCTATCAAGAAAT	1020
DB	961	GTGCAATTCCTGCAATCTCTGTCTGCAAGAAATGAGGCAAAATGCTATCAAGAAAT	1020
QY	1021	CAATAAAGATATCTCTGTCTGCAAGCGCATATCTCTGCAATTCAGATGATGCTCTG	1080
DB	1021	CAATAAAGATATCTCTGTCTGCAAGCGCATATCTCTGCAATTCAGATGATGCTCTG	1080
QY	1081	GTGACAGCAGCTAGATATCTGCAAGAGCGGCAAGTTCCTGCAATTCAGATGATGCTCTG	1140
DB	1081	GTGACAGCAGCTAGATATCTGCAAGAGCGGCAAGTTCCTGCAATTCAGATGATGCTCTG	1140
QY	1141	ACCGATATCTTCTGATGATGCTGCAAGAGCGGCAAGTTCCTGCAATTCAGATGATGCTCTG	1200
DB	1141	ACCGATATCTTCTGATGATGCTGCAAGAGCGGCAAGTTCCTGCAATTCAGATGATGCTCTG	1200
QY	1201	CGCTATATCAATTCCTGATGATGCTGCAAGAGCGGCAAGTTCCTGCAATTCAGATGATGCTCTG	1260
DB	1201	CGCTATATCAATTCCTGATGATGCTGCAAGAGCGGCAAGTTCCTGCAATTCAGATGATGCTCTG	1260

```

RES0112
AA172146
ID      AA172146 standard; cDNA: 1257 BP.
XX
XX      AC
XX      AA172146;
DE      25-MAR-2002 (first entry)
XX
DE      cDNA encoding ER splice variant ER-alpha.
XX
KW      DNA binding domain; DBD; ligand binding domain; LBD; chimeric receptor;
KW      estrogen receptor; ER; chromosome 14; ER-alpha; ER-beta; exon 8; PCR;
KW      estradiol; nuclear receptor; ER-estrogen receptor; amplified protein;
KW      polymerase chain reaction; AF-2 region; splice variant; SS.
XX
OS      Homo sapiens.
XX
XX      Key
FH      Location/Qualifiers
FI      chr5
FI      1:1257
FI      /*tag=
FI      /product="ER-alpha"
XX
XX      BP162264-AZ.
XX
XX      12-DEC-2001.
XX
XX      25-MAR-1997; 2001EP-020021.
XX
XX      26-MAR-1996; 96EP-0200820.
XX      22-NOV-1996; 96EP-0201884.
XX      25-MAR-1997; 97EP-0200903.
XX
XX      (ALKU ) AKZO NOBEL. NV.
XX
XX      MosseIman S, Dijkema R.
XX
XX      WPI: 2002-084414/12.
XX      P-PsDH; AAB47836.
XX

```

New isolated chicken ER receptor cDNA comprising a DNA binding domain and/or ligand binding domain of a new estrogen receptor, for identifying functional ligands or hormonal analogs for the receptor.

Example B; Page 23; 45pp; English.

The sequences given in AAI72146 and AAI72153 encode splice variants of a novel estrogen receptor (ER). The gene encoding this new ER is located on chromosome 14 and has a different tissue distribution from classical ER. This ER also has two orphan ER's, ER-alpha and ER-beta. These orphan receptors have estrogen receptor related structure but do not appear to be able to bind estradiol or other ER ligands. These splice variants differ from the parent ER around exon 8. One clone contains exon 8B through alternative splicing. This causes an immediate termination of the reading thereby creating a truncation at the carboxy terminus. The other splice variant contains an alternative exon 8, exon 8C, which encodes two C-terminal amino acids and then has a stop codon. The splice variant proteins do not contain the AF-2 region and therefore probably lack the ability to modulate transcription of target genes in a ligand dependant manner. However they may be able to interfere with the functioning of the WT classical ER or the novel ER of the invention, either by heterodimerisation or by occupying estrogen response elements or by interactions with other transcription factors.

	Sequence	1257 BP;	297 A;	327 C;	355 G;	278 T;	0 other:
Query Match	100.0%;	Score 1257;	DB 24;	Length 1257;			
Best Local Similarity	100.0%;	Pred. No. 0;					
Matches 1257;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps 0;
CY	1 ATGAATTCACAGATTCCCGGCAATGTCTACTTACCTGGAAAGTGCGCTGGTTGGGACACC	60					
DB	1 ATTGAATTAATCATTTCCGCAATGTCTACTTACCTGGAAAGTGCGCTGGTTGGGACACC	60					
CY	61 ACACAGCCCAAGAATGTCTTGCTGCACACAGCGGCACTTCTCTTATGGTCAATCAC	120					
DB	61 ACAAGGCCAAGAATGTCTTGCTGCACACAGCGGCACTTCTCTTATGGTCAATCAC	120					
CY	121 CAATTATTCATCTGATGTGGGAAATCTCAAAGATCTTGCTGGTGAAGTAATATGGCTA	180					
DB	121 CAATTATTCATCTGATGTGGGAAATCTCAAAGATCTTGCTGGTGAAGTAATATGGCTA	180					
CY	181 GAACCAACGCTACGCTGTACACAGAACACATCTGAAGCAAGGCTTGTATCGCAAGCTCTG	240					
DB	181 GAACCAACGCTACGCTGTACACAGAACACATCTGAAGCAAGGCTTGTATCGCAAGCTCTG	240					
CY	241 GTATATCTCTGTTATCTGTTAAATGAGTAATCTTATCTGCTATCTGCTATCTGCTAT	300					
DB	241 GTATATCTCTGTTATCTGTTAAATGAGTAATCTTATCTGCTATCTGCTATCTGCTAT	300					
CY	401 GATTATGCTATCGCATATCACTATGGAAGCTCTGGTGTGTAAGATAATGAGGCTTTTTT	360					
DB	401 GATTATGCTATCGCATATCACTATGGAAGCTCTGGTGTGTAAGATAATGAGGCTTTTTT	360					
CY	461 AAAGCAAGCATTCGAAGCATTAATATATTTTGTGCATCTATCAATACAGTAGCATCT	420					
DB	461 AAAGCAAGCATTCGAAGCATTAATATATTTTGTGTGCTATCAATACAGTAGCATCT	420					
CY	481 ATGGTCAAGCTGGGCTGTGCGGAGATATGAGAGCTGGGTAAGGCTTATGGGAGAAATANA	540					
DB	481 ATGGTCAAGCTGGGCTGTGCGGAGATATGAGAGCTGGGTAAGGCTTATGGGAGAAATANA	540					
CY	541 ACTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT	600					
DB	541 ACTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT	600					
CY	601 CGAGTGTGGAGATGT	660					
DB	601 CGAGTGTGGAGATGT	660					


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UY 721 ATGATGATGCTGCTGACAAATTTGGCGACAAAGATTGTGAAACATATGATGCTGGGCTG 780
DB 721 ATGATGATGCTGCTGACAAATTTGGCGACAAAGATTGTGAAACATATGATGCTGGGCTG 780
UY 781 AAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 AAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
UY 841 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
UY 901 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
UY 961 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 961 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
UY 1021 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
UY 1081 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
UY 1141 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
UY 1201 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 TGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

```

```

DB 721 2002-084414/12.
DB P PSDB: AAB47847.
XX
PT New isolated chimeric receptor comprising a DNA binding domain and/or
PT ligand binding domain of a new estrogen receptor, for identifying
PT functional ligands or hormonal analogs for the receptor
XX
PS Example B: Page 13: 35pp: English.
XX
CC The sequences given in AAI72146 and AAI72153 encode splice variants
CC of a novel estrogen receptor (ER). The gene encoding this new ER is
CC located on chromosome 14 and has a different tissue distribution from
CC classical ER. This ER also has two orphan ERs, ER-alpha and ER-beta.
CC These orphan receptors have estrogen receptor related structure but do
CC not appear to be able to bind estradiol or other ER ligands. These
CC splice variants differ from the parent ER around exon 8. One clone
CC contains exon 8B through alternative splicing. This causes an immediate
CC termination of the reading thereby creating a truncation at the carboxy
CC terminus. The other splice variant contains an alternative exon 8, exon
CC 8C, which encodes two C-terminal amino acids and then has a stop codon.
CC The splice variant proteins do not contain the AF-2 region and therefore
CC probably lack the ability to modulate transcription of target genes in
CC a ligand dependant manner. However they may be able to interfere with
CC the function of the WT classical ER or the novel ER of the invention,
CC either by heterodimerisation or by occupying estrogen response elements
CC or by interactions with other transcription factors.
XX
SO Sequence 1251 BP: 297 A: 324 C: 354 G: 276 T: 0 other:
Query Match 99.48% Score 1249; DB 24; Length 1251;
Host Local Similarity 100.00%; Pred. No. 0;
Matches 1249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 1 ATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB 1 ATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
UY 61 ACAAAGCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 ACAAAGCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
UY 121 CAGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 CAGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
UY 181 GAAACACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 GAAACACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
UY 241 GAAACACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GAAACACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
UY 301 GATTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 GATTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
UY 361 AAAAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 AAAAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
UY 421 GATAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GATAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
UY 481 AAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 AAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
UY 541 AAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 AAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

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UY 781 AAGAGATTCGGAGCTTGTGAGTACGCTGTGCAACGATGCGTCTCTGAAAG 840
DB 781 AAGAGATTCGGAGCTTGTGAGTACGCTGTGCAACGATGCGTCTCTGAAAG 940
UY 841 TTTTATATGATGATTTTATATATATATATATATATATATATATATATATAT 900
DB 841 TTTTATATGATGATTTTATATATATATATATATATATATATATATATATAT 900
UY 901 CTGATCTTTTGTATATATATATATATATATATATATATATATATATATATAT 960
DB 901 CTGATCTTTTGTATATATATATATATATATATATATATATATATATATATAT 960
UY 961 CTGATATCTTGTATATATATATATATATATATATATATATATATATATATAT 1020
DB 961 CTGATATCTTGTATATATATATATATATATATATATATATATATATATATAT 1020
UY 1021 GATTAATATATATATATATATATATATATATATATATATATATATATATAT 1080
DB 1021 GATTAATATATATATATATATATATATATATATATATATATATATATATAT 1080
UY 1081 GTTATATATATATATATATATATATATATATATATATATATATATATATAT 1140
DB 1081 GTTATATATATATATATATATATATATATATATATATATATATATATATAT 1140
UY 1141 AATGATATATATATATATATATATATATATATATATATATATATATATATAT 1200
DB 1141 AATGATATATATATATATATATATATATATATATATATATATATATATATAT 1200
UY 1201 GCGTATGCTTACCTGTTATATATATATATATATATATATATATATATATAT 1247
DB 1201 GCGTATGCTTACCTGTTATATATATATATATATATATATATATATATATAT 1247

RESULT 6
AA172128
ID AA172128 standard; cDNA: 1434 BP.
AC AA172128;
XX
DI 25-MAR-2002 (first entry)
XX
DE Estrogen receptor cDNA.
XX
KW DNA binding domain; DBD; ligand binding domain; LBD; chimeric receptor;
KW estrogen receptor; ER; chromosome 14; ER-alpha; ER-beta; xmr-B.
XX
KW estradiol; nuclear receptor; progesterone receptor; ss.
XX
XX Homo sapiens.
XX
XX Key: Logat for quality
XX FT CDS 1..1434
XX FI /Atag: a
XX FI /Product: "ER"
XX
XX EP1162264-A2.
XX
XX 12-DEC-2001.
XX
XX 25-MAR-1997; 2001EP-009001
XX
XX 26-MAR-1997; 96EP-0200820
XX 22-NOV-1996; 96EP-0203284.
XX 25-MAR-1997; 97EP-0209903.
XX
XX (ALU) AK20 NOBEL NV.
XX
XX Mosselman S. Dijkema R.
XX
XX WP1: 2002 084414/12.
XX p-PSDB: AAB47834.
XX
XX New isolated chimeric receptor comprising a DNA binding domain and/or
XX ligand binding domain of a new estrogen receptor. For identification

```

```

PI functional ligands or hormonal analogs for the receptor
XX
XX Example A: Page 12: 35pp; English.
PS
XX This sequence encodes a novel estrogen receptor (ER). The gene encoding
CC this new ER is located on chromosome 14 and has a different tissue
CC distribution from classical ER. This ER also has two orphan ER's,
CC ER-alpha and ER-beta. These orphan receptors have estrogen receptor
CC related structure but do not appear to be able to bind estradiol or other
CC ER ligands. The DNA binding domain (DBD) and ligand binding domain (LBD)
CC from this ER may be used in the chimeric receptor of the invention
CC which also has an N-terminal domain. The chimeric receptor, or DNA
CC encoding it, is useful in a screening assay for identification of new
CC drugs. Similar chimeric receptors comprising the LBD of the new ER,
CC and also comprising the DBD and an N-terminal domain are useful for the
CC screening of compounds to identify new ligands or hormone analogs which
CC are able to activate the new ER. Chimeric receptors comprising a DBD
CC of the new ER, and LBD and an N-terminal domain derived from
CC another nuclear receptor, can be used to identify new ligands or
CC hormone analogs for the nuclear receptors.
XX
XX Sequence 1434 BP; 347 A; 373 C; 406 G; 308 T; 0 other:
SU
XX
XX Query Match 99.2%; Score 1247; DN 24; Length 1434;
XX Host Local Similarity 100.0%; Prod. No. 0;
XX Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGAAATTAAGGATTCGAGCAATGCACTACCTGGAAGCTGCTGGTGGAGAGAC 60
DB 1 ATGAAATTAAGGATTCGAGCAATGCACTACCTGGAAGCTGCTGGTGGAGAGAC 60
XX
XX 61 ACAAGTCAATATGTTTGTGGGCAACAGCTGGGAGCTTTTGTCTTATATGTTATG 120
DB 61 ACAAGTCAATATGTTTGTGGGCAACAGCTGGGAGCTTTTGTCTTATATGTTATG 120
XX
XX 121 CAGTTATGACATGCTGATGCGAAGCTGAAAGAGTCTGCTGCTGCAAGATGCTA 180
DB 121 CAGTTATGACATGCTGATGCGAAGCTGAAAGAGTCTGCTGCTGCAAGATGCTA 180
XX
XX 181 GAACACACCTTACCTGTTAAATACAGACACTTAAAGAGAGGTTACTGGAAATCG 240
DB 181 GAACACACCTTACCTGTTAAATACAGACACTTAAAGAGAGGTTACTGGAAATCG 240
XX
XX 241 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
XX
XX 301 GATTAGGATGCGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 GATTAGGATGCGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 360
XX
XX 361 AAAAGAGAGATTGAAATGATATATATATATATATATATATATATATATATAT 420
DB 361 AAAAGAGAGATTGAAATGATATATATATATATATATATATATATATATATAT 420
XX
XX 421 GATTAATATATATATATATATATATATATATATATATATATATATATATATAT 480
DB 421 GATTAATATATATATATATATATATATATATATATATATATATATATATATAT 480
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XX 481 ATGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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XX 541 ACTGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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[illegible]

9D	20-JUN-2002
XX	14-DEC-2001; 2001WA-JP10998.
XX	
XX	14-DEC-2000; 2000JP-0380427.
PR	40-JAN-2001; 2001AP-0022105.
XX	
XA	(GLYX) GLYPHOS OPTICAL CO LTD.
XX	
PI	Kato N., Sakamoto H;
OR	WPI; 2002-628176/56.
DR	P PDB; ABB80756.
PT	Autorrection function-embedded confocal optics-based fluorometric analyzers for studying behaviors of fluorescence-labeled molecules particularly intracellular biological molecules like proteins at molecular level -
XX	
TS	
XX	Example 2; Page 98-105; 109pp; Japanese.
CC	The invention relates to a fluorometric analyzer that comprises a laser light source, an optical system for focusing the light beam from laser light source to a sample to form a confocal region, another optical system for focusing fluorescence from the sample, a light detector for measuring intensity, and a recording means to record the variation of intensity in the measured fluorescence. The analyzers are for studying behaviors of fluorescence-labeled molecules particularly intracellular biological molecules like proteins at molecular level, e.g. protein functions and interactions. Such analyzers are stable and convenient to operate, thereby enabling easy performance of fluorescence correlation spectroscopy, fluorescence intensity distribution analysis and fluorescence intensity multiple distribution analysis. The present sequence represents the nucleotide sequence of a fusion gene comprising a GFP (green fluorescent protein) gene and hER (human estrogen receptor) beta gene.
CC	
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SD	Sequence: 2433 bp; 587 A; 704 C; 659 G; 483 T; 0 other;
Query Match	99.28; Score 1247; Len: 2433
Best Local Similarity	100.0%; Freq. No. 0;
Matches 1247:	Conservat: 0; Mismatch: 0; Indels: 0; Gaps: 0;
QY	I ATGATTTAAGCATTTCGACATGTCTCAATCTTGAATCTTGAAAGTGGGTCAGGC 60
DB	
956	ATTAATTAAGCATTCAGCAATGCTACTAACTGCAAGTGGGTCAGGC 1015
DB	
1016	ATGAAGGCAATGTCTTGTGCGAACACCTGGCACTTCTTACTGCTGTCAGGC 1075
QY	61 ATGAAGGCAATGTCTTGTGCGAACACCTGGCACTTCTTACTGCTGTCAGGC 120
DB	
1076	GACTTATTCATCTATGCGCAACCTCAAAAGCTCTGCTGTAAGTATGCTA 180
DB	
181	GAAATACCTTCTACTGTTAAATGCAACAACATCAAAAAGCAAGCTTGAAGCTGCT 240
DB	
1146	GAAACACCTTACCTGTTAAATGCAACAACATCAAAAAGCAAGCTTGAAGCTGCT 1195
QY	241 GTTATCTTCTTACTGCTGCAAGCTTCAAAAGCAAGCTCTATCTGCTGCTGCT 300
DB	
1196	GCTATCTTCTTACTGCTGCAAGCTTCAAAAGCAAGCTCTATCTGCTGCTGCTG 1255
QY	401 GATATCTGCTGCTGCAAGCTTATGCAAGCTCTGCTGCTGCAAGCAATGTAAGCTCTTCT 460
DB	
1256	GATTGCTATGCTGCAATGCTATGCAAGCTCTGCTGCTGCAAGCAATGTAAGCTCTTCT 1415
QY	461 AAAATAGATTCGAAGAATCAATGATTAATTTGCTCACTGACAAATATAGTAGAATC 420
DB	
1416	AAAAAGATTCGAAGAATCAATGATTAATTTGCTCACTGACAAATAGTAGAATC 1475
QY	421 GAATAAAGATTCGATGACAGCTGCCAGCTTGTCAATTCGCAAGCTGTAATCAAGTGGCA 480
DB	

[illegible][illegible]

[illegible]

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RES011_27
AA92174
ID   AA92174 standard; cDNA; 1728 bp.
XX
XX   AA92174:
XX
XX   05-JAN-2001 (first entry)
XX
XX   cygias lapides oestrogen receptor encoding RNA SP0 ID N002.
XX
XX   cygias lapides; oestrogen receptor; ds.
XX
XX   cygias lapides.
XX
XX   JF2000201688-A.
XX
XX   25-JUL-2000.
XX
XX
XX   06-APR-1999; 94JP 0098787.
XX
XX
XX   10-NOV-1998; 9BJP-0319465.
XX
XX
XX   (SUMO ) SUMITOMO CHEM CO LTD.
XX
XX   WPJ: 2000-567950/53.
XX
XX   P-PDBJ: AAB20897.
XX
XX
XX   An estrogen receptor gene and its application -
XX
XX   Claim 3; Page 11-13; 23pp; Japanese.
XX
XX
XX   The present sequence encodes an estrogen receptor derived from
XX   cygias lapides. Also described are: (1) a vector comprising the
XX   estrogen receptor gene; (2) a transformant prepared by introducing
XX   the estrogen receptor gene or vector from (1) into a host cell;
XX
XX   (3) a method for the preparation of an estrogen receptor comprising
XX   culturing the transformant from (2) to produce the estrogen receptor;
XX   and (4) a method for the evaluation of estrogen receptor activating
XX   ability of a chemical substance in which the chemical substance is
XX   reacted with a transformant prepared by introducing a reporter gene
XX   connected downstream of a transcription controlling region containing
XX   an estrogen response sequence and the above estrogen receptor gene to
XX   an estrogen-responsive host cell. The transformant can be used for
XX   the evaluation of estrogen receptor-activating ability of a chemical
XX   substance.
XX
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XX   Sequence 1728 BP; 378 A; 514 C; 497 G; 339 T; 0 other;
XX
Query Match          26.4%; Score 152.4; Dh 21; Length 1728;
Host Local Similarity 61.4%; Prod No. 2,2e+77;
Matches 628; Conservative 0; Mismatches 446; Indels 48; Gaps 4.

274 GAAGCTACTTGTGACGGTCGTCAGACATTAACAATCATCAATATCAATATCAATGCG 333
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Eh    GAACAGCGATTGTGCAGCCGTTGAGCAGGACAGCAAGCGTGCTGGAGTAGCATGCTGGTGGTGG 468
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

334 TTGTGTGAAGCATGTAAAGCCCTTTTTTAAAGAAGCATTTAAGACATAATCATTAAT 393
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Eh    TTTTGTGAGAGGCTGTAAAGGCCCTTTTTTAAAGAAGCATTTAAGACATAATCATTAATG 528
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

494 TGTCGACATCAAAATGACATGTTCATATGATAAAAGGCGGCTGTAATGTGCAAGCGTGT 453
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

454 CAATTCGAAATGTTTAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA 494
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Eh    CGCTTAGGAAATGTTTAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAAT 648
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495 -----CTTCGAGAGAGAGAGATGTGGTACAGCGCTTGTGGAGGATAGATATGTCGAG 549
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Eh    CTTCATTTTAAAGGCTGTAAGAGGAGGAGAGAGCGCTGTGATGATGTAAGCAAGATGTAAAG 708
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Target activated nucleic acid biosensor: signaling moiety: human
nucleic acid sensor: detection: engineering: drug optimization:
estrogen receptor: gene: ss

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

AM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 00:20:22; execution time 09.1900 seconds.

Title: US-08-826-261A-200
Portect score- 1357

Sequencia:

ATGAA TTA CAG CATT C C A C C

СЪСТАВИТЕЛСТВО

Summary table

apop 10.0 , capext 1.0

Search time: 441362 secs, 153338381 residues

Total number of hits satisfying chosen parameters: 622724

Maximum job seq length: 2000000000

Post-processing: Minimum Match 0%

listing first 120 summaries

Pat abuse :

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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	1	1.247	99.2	1469	2	US-08-836-620A-4	Sequence 4, Appl	
	2	1.247	99.2	1647	4	US-09-139-0-17-2	Sequence 2, Appl	
	3	1.247	99.2	1647	4	US-09-561-741A-2	Sequence 2, Appl	
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	5	9.922	73.4	1458	2	US-08-836-620A-6	Sequence 6, Appl	
	6	3.22	25.6	4563	1	US-08-076-726-16	Sequence 16, Appl	
	7	3.22	25.6	4563	1	US-08-260-452-9	Sequence 9, Appl	
	8	3.22	25.6	4563	2	US-08-481-720-9	Sequence 9, Appl	
	9	3.22	25.6	4563	2	US-08-897-719-9	Sequence 9, Appl	
	10	3.22	25.6	4563	4	US-09-163-269-3	Sequence 9, Appl	
	11	320.4	25.5	6450	4	US-09-041-886-34	Sequence 34, Appl	
	12	420.4	25.6	6450	7	US-08-453-198-1	Sequence 36, Appl	
	13	216.8	17.2	1456	3	US-08-693-440-2	Sequence 2, Appl	
	14	216.8	17.2	1456	4	US-08-566-660-2	Sequence 2, Appl	
	15	216.8	17.2	2122	3	US-08-574-264-2	Sequence 2, Appl	
	16	113.8	9.1	1615	3	US-09-040-508-1	Sequence 2, Appl	
	17	113.8	9.1	1615	3	US-09-500-554-1	Sequence 1, Appl	
	18	95.2	7.6	3115	4	US-06-241-846-10	Sequence 1, Appl	
	19	89	7.1	6244	1	US-08-076-726-15	Sequence 15, Appl	
	20	84	7.1	6244	1	US-08-260-452-8	Sequence 15, Appl	
	21	99	7.1	6244	2	US-08-481-970-8	Sequence 8, Appl	
	22	83	7.1	6244	2	US-08-897-719-9	Sequence 8, Appl	
	23	84	6.7	6244	4	US-09-163-269-8	Sequence 8, Appl	
	24	84.8	6.7	6127	4	US-08-479-914-1	Sequence 8, Appl	
	25	84.8	6.7	7257	4	US-09-091-042A-1	Sequence 1, Appl	
	26	81	6.4	4014	1	US-08-629-439-1	Sequence 1, Appl	
	27	81	6.4	4014	1	US-08-759-873-1	Sequence 1, Appl	

28	80.8	6.4	1574	6	5240433-1	Patient No. 5240433-1
29	78	6.2	2599	6	5232696-1	Patient No. 5232696-1
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31	74.4	5.9	2658	2	US-08-592-384-3	Sequence 3, Appl1
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36	74.4	5.9	4036	6	US-08-096-6594-52	Sequence 52, Appl1
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39	74.4	5.9	4460	3	US-08-312-312A-1	Sequence 1, Appl1
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42	72.8	5.8	2067	4	US-09-106-194-11	Sequence 11, Appl1
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57	64	5.1	1245	4	US-09-510-654-3	Sequence 3, Appl1
58	64	5.1	1245	4	US-09-510-654-3	Sequence 3, Appl1
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60	64	5.1	2330	4	US-09-510-654-7	Sequence 7, Appl1
61	64	5.1	2027	2	US-09-132-619-9	Sequence 9, Appl1
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85	59	4.7	1277	5	US-08-372-652-14	Sequence 14, Appl1
86	59	4.7	1677	5	PCT-0599-16311-14	Sequence 14, Appl1
87	59	4.7	1787	5	US-08-372-652-6	Sequence 6, Appl1
88	59	4.7	1787	5	PCT-0597-16311-6	Sequence 6, Appl1
89	58.8	4.7	1748	1	US-08-255-471-8	Sequence 8, Appl1
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91	56.8	4.5	1534	4	US-08-653-6486-2	Sequence 2, Appl1
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97	54.4	4.3	1518	4	US-07-128-142-3	Sequence 3, Appl1
98	54.4	4.3	1608	3	US-09-484-245-5	Sequence 3, Appl1
99	54.4	4.3	1608	3	US-09-514-247-5	Sequence 5, Appl1
100	54.4	4.3	1844	4	US-08-134-5570-1	Sequence 1, Appl1


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1  RESULT 15
2  US-08-564-264-2
3  ? Sequence 2, Application US/08564264
4  ? Patent No. 6040430
5  ? GENERAL INFORMATION:
6  ? APPLICANT: STEWART, FRANCIS
7  ? TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC
8  ? TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC RECOMBINASE/NUCLEASE
9  ? TITLE OF INVENTION: RECEPTOR FUSION PROTEINS
10 ? NUMBER OF SEQUENCES: 2
11 ? CORRESPONDENCE ADDRESS:
12 ? ADDRESSEES: NIKALDO, Marmolestein, Murray & Oram
13 ? STREET: 655 Fifteenth Street N.W., Suite 340

```

```

1 CITY: Washington
2 STATE: D.C.
3 COUNTRY: U.S.A.
4 ZIP: 20005-5701
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patchfile Release #1.0, Version #1.10
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/564,264
14
15 FILING DATE:
16 CLASSIFICATION: 435
17
18 PRIOR APPLICATION DATA:
19 PRIOR APPLICATION NUMBER: PCT/EP94/02088
20 FILING DATE: 28-JUN-1994
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: EP 93 110 298.2
24 FILING DATE: 28-JUN-1993
25
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Murray, Robert R.
28 REGISTRATION NUMBER: 22,980
29 REFERENCE/CHECK NUMBER: P564-5019
30
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (202)638-5000
33 TELEFAX: (202)638-4810
34
35 INFORMATION FOR SEQ ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 2322 base pairs
38 TYPE: nucleic acid
39 STRANDNESS: single
40 TOPOLOGY: linear
41
42 FEATURE:
43 NAME/KEY: misc_feature
44 LOCATION: (1-1269)
45 OTHER INFORMATION: /note="FLP recombinase domain."
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47 FEATURE:
48 NAME/KEY: misc_feature
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52 FEATURE:
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54 LOCATION: (1285-2322)
55 OTHER INFORMATION: /note="Estrogen binding domain."
56
57 US-08-564,264-2
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59 Query Match: 17.2%; Score 216.8; BB 3; Length 2322;
60 Best Local Similarity 61.3%; Pred. No. 5e-48;
61 Matches 385; Conservative 0; Mismatches 257; Indels 5; Gaps 2;
62
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COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
CONTAINER: 100 disk

OPERATING SYSTEM: PC-LOS/MS-DOS

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1  COL AMOUNT:  AMOUNT IN INCREASE:  71.00  VOL IN STOCK:  71.20
2
3  CURRENT APPLICATION DATA:
4

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APPLIATION NUMBER: 05/09/041,886

FILING DATE:

CLASSIFICATION;
;
; TECHNOLOGY/AGENT INFORMATION.

NAME: Campbell, Cathryn A.

REFERENCE/DOCKET NUMBER: P-LJ 2626

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

NAME/KEY:	CDS
NAME/KEY:	CDS

HS-09-041-886-10

Query Match 7.68; Score 95.2; DB 4; Length 3715;

Best Local Similarity	51.28;	Pred. NO. 1e-15;							
Matches	337.	Conservative	0.	Mismatches	298.	Indels	18.	Gaps	4.

OF COURTESY OF THE

[illegible][illegible]

DB 0267 0102AAGGTCCTGTCAAAAGACGGCGTGAAGGSAATCAAGATACCTTGCTGGCCAGCAGCAG 2421

405 AATCAGTGTAAATCGATAAAATCGCGCAAGACCTGGCAGCGCTTCGGACTTCGGAA 464

2322 AATGATTGCCTATTGATAAATCGGACGAAATTCGATCTCTCTCTTTGGAA 2381

465 GTCTACCAATGGTAATCTGAATCTGGTTCGCAACAGATATATGGTACCCCT 524

0383 ATTTATCGAACGACGATGACCTCTGGCAAGCTTGGTAATCTGAA 3441

.....

[illegible][illegible]

2501 AGCTGACAGTUTTCACACATTGAAGCTATGAAATG-----TTAGCTCCATCTTTCTG 2550

645 AGIGCTCACTCTCTGGAGGCTGAGGGCGCCCATTTCTGATCACTGGCGCAATGGCG 704

[illegible]

705 CTTACCGAGGCTTCATGATGATCTCCCTGACCAGTTCGCGAAGAGGATTCGTAA 764

[illegible]

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[illegible][illegible]

825 GCGGCTC TGGAGAGTTC TGGATGGACGTGTAA TGA TGCGGC TGA GTGGCG----- 8/8

Dh 2730 GCGCTCTCAATTCAGIAATCTTGATGCGCTCATGCTGTTGATGCGCTGCGGACCTT 2789

100

APPLICANT: Gossen, Manfred
 APPLICANT: Bujard, Hermann
 APPLICANT: Salfeld, Jochen
 APPLICANT: Voss, Jeffrey
 TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controllable
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lathive & Cockfield
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,970
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/260,452
 FILING DATE: 14-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076,427
 FILING DATE: 14-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Giulio A. DeConti, Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/EXCERPT NUMBER: R81-013P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6244 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Human cytomegalovirus
 STRAIN: Towne (hcmv)
 IMMEDIATE SOURCE:
 CLONE: pHD BGR3

[illegible]

Patent No. 592927

GENERAL INFORMATION:

APPLICANT : Gossen, Manfred

APPLICANT : Bugard, Hermann

APPLICANT : Salfer, Jochem

APPLICANT : Voss, Jeffrey

TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotic

TITLE OF INVENTION: Cells by Tetraacycline-responsive promoters

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-XTS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/897,719

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/260,452

FILING DATE:

APPLICATION NUMBER: 08/076,327

FILING DATE: 14-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Giulio A. Decortis, Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BRI-0130P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 6244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Human cytomegalovirus

STRAIN: Towne (HCMV)

IMMEDIATE SOURCE:

CLONE: pUHD BGR3

US-08-897-719-8

[illegible]

RESULTAT 23


```

1 CLASSIFICATION: 435
2 ATTORNEY/AGENT INFORMATION:
3 NAME: KIT, Gordon
4 REGISTRATION NUMBER: 40,764
5 ALTERNATE/DOCKET NUMBER: A-6612
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (202) 293-7060
8 TELEFAX: (202) 293-7860
9 INFORMATION FOR SEQ ID NO: 1:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 404 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: cDNA
16 HYPOTHEICAL: NO
17
18 US-08-629-939-1
19
20 Query Match 6.4%; Score 81; DB 1; Length 404;
21 Best local similarity 63.7%; Pred. No. 5,4e-12;
22 Matches 123; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
23
24 Y 293 TTGTGAGGATTACATCGGGGATATCATATGATCTGGTGTGTGAGAGATTACG 352
25 1841 TTGTGGGTAATAAATAGGATGCTATATGCTGTCTTAACTGTAAGAGCTTAGG 1940
26 Y 353 CCTTTTAAAGAGCAATTCAGGCAATTAATATATTTCTAGCTACAAATAGT 412
27 Db 1941 TTTTCTTTTAAAGGCGGATGGAAGGGAGGACCAACTAGTATGTGTGAAAGAAATAGT 2000
28 Y 413 CTACATATCATAAAGCTGGGAGACAGCTGGGACGGCTGGCTGGCTGGAGTTAGG 472
29 Db 2001 GAATCTTATATATAATATCTCTGAGAAAAATCTCTTAAATATCTGCTTAAAGTCTCTGT 2060
30 Y 473 AATTCAGAGATGT 485
31 Db 1 1 1 1 1 1 1 1 1 1
32 2061 ACCCTGGCATGCT 2073
33
34 RESULT 27
35 US-08-759-873-1
36 : Sequence 1, Application US/08759873
37 : Patent No. 5683885
38
39 GENERAL INFORMATION:
40 APPLICANT: Kieback, Dirk G.
41 TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
42 NUMBER OF SEQUENCES: 14
43 CORRESPONDENCE ADDRESS:
44 ADDRESSEE: SINGER, MICHAEL ZINN, MACHAK & SPAS
45 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
46 CITY: Washington, D.C.
47 STATE: D.C.
48 COUNTRY: U.S.A.
49 ZIP: 20037
50
51 COMPUTER READABLE FORM:
52 MEDIUM TYPE: Floppy disk
53 COMPUTER: IBM PC compatible
54 OPERATING SYSTEM: PC-DOS/MS-DOS
55 SOFTWARE: Patent to Release #1.0, Version #1.25
56 CURRENT APPLICATION DATA:
57 APPLICATION NUMBER: US/08759, 873
58 FILING DATE: 12-APRIL-1996
59 CLASSIFICATION: 435
60 ATTORNEY/AGENT INFORMATION:
61 NAME: KIT, Gordon
62 REGISTRATION NUMBER: 40,764
63 REFERENCE/DOCKET NUMBER: A-6612
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: (202) 293-7060
66 TELEFAX: (202) 293-7860
67 INFORMATION FOR SEQ ID NO: 1:
68 SEQUENCE CHARACTERISTICS:

```



```

1 LENGTH: 304 base pairs
2 TYPE: nucleic acid
3 STRANDEDNESS: single
4 TOPOLOGY: linear
5 MOLECULE TYPE: cDNA
6 HYDROTHERMAL: NO
7 INS-OR 759-874 1

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Query Match	6.48;	Score 81;	DB 1;	Length 3014;
Host Local Similarity	64.7%;	Prod. No. 5,40512;		
Matches 123;	Conservative	0;	Mismatches 70;	Indels 0;
				Gaps 0;

[illegible]

27	47	AACTTCGAGANTGCT	485
105	205	ACCTCTCTGATGCT	2075

```

RESOLVE 28
%260432.1
PATENT No. %260432
APPLICANT: TAKAKU, FUMIMARU; ISHIKAWA, TAKASHI; IMAMOTO, MICHIO;
EVANS, RONALD M.; JIMESINO, KAZUHIKO
TITLE OF INVENTION: HUMAN GAMMA BELLINOT ACID RECEPTOR DNA
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/07/470,407
FILING DATE: 22 JUS-1989
SEQ ID NO: 1
LENGTH: 1576
%260432.1

```

Query Match	6.48;	Score 80.8;	DB 6;	Length 1576;
Best Local Similarity	62.38;	Prod. No. 4.7e-12;		
Matches 121;	Conservative	0;	Mismatches 77;	Indels 0;
				Gaps 0;

[illegible]

UY 446 TGTTCCTAAGTGGCGATTCGTCGAAC; 489
 1111111111111111 111
UB 647 TGCCTTCGAAGCTGGAGCACTCCTCAAC; 670

RESUME 29
 522606 1
 Author No. 522606
 APPLICANT: BERAUDIN DE THE, HUGHES, MARCITTO, AGNES, FLORENTS,
 PIERRE-DEJEAN, ANNE
 TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR RELATED
 PROTEIN IMMUNOPROTEIN EXPRESSED IN HUMAN HEPATOCYTOBLAST CARCINOMA
 NUMBER OF SEQUENCES: 11
 CURRENT APPLICATION DATA:

```

1  APPLICATION NUMBER: US/07/14,130
2  FILING DATE: 17 DEC 1987
3  PRIOR APPLICATION DATA:
4  SEQ ID NO: 1
5  LENGTH: 2989
6  5224606-1

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Query Match 6.28; Score 78; Path 6; Length 2889;
 Host Local Similarity 61.98; Prod. No. 3.4e-11;
 Matches 140; Conservative 0; Mismatches 85; Indels 1; Gaps 12

[illegible]

404 AGTCTTATCAAGTTCGCAATGGTGAAGTTCGGCTCTCTGAAAGAGAGG 509
 740 AGTCTTTGCAAGTACGAAATCTCTAAAGAAATCTGAGAAATATGAAAG 785

RESULT: 40
US-09-277-078-1
1. Sequence: 1, Application: US/09/277/078
2. Patent No.: 6,312,949
3. GENERAL INFORMATION:
4. APPLICANT: Sakurada, Kazuhito
5. APPLICANT: Palmer, Theo
6. APPLICANT: Iddes, Fred H.
7. TITLE OF INVENTION: REGULATION OF TYROSINE HYDROXYLASE
8. TITLE OF INVENTION: EXPRESSION
9. FILE REFERENCE: 07/251/031001
10. PARENT APPLICATION NUMBER: 05/091,277, 078
11. CURRENT FILING DATE: 1999-04-26
12. NUMBER OF SEQ. ID NOS.: 60
13. SOFTWARE: FastSeq for Windows Version 4.0

```

1 LENGTH: 1797
2 TYPE: DNA
3 ORGANISM: Ratfus norvegeicus
4
5 FEATURE:
6
7 NAME/KEY: CDS
8 LOCATION: (1) ... (900)
9 OS: 09-277-078-1

```

Query Match	5, 98;	Score	74.4;	DB	4;	Length	1797;
Best Local Similarity	57.98;	Prod. No.	2, 50-10;				
Matches	142;	Conservative	0;	Mismatches	96;	Indels	0;
				Gaps	0;		

[illegible]

O7 404 AGCTTTACGAAAGTACCAATCGCTAAGTCGCATCTTGAGAGAACAA 511
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O8 965 AGCTGCTGGCTGTCCGAGTCGTAAACAATCGCTTCGAACGGAATT 1012

RESULT 31
US-08-592-483-3
Sequence 3, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: Tsai, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Polynucleotide Acids"
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 900 Pacific First Centre, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2MB storage
COMPUTER: IBM PC/486 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows 5.01-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/BOOKET NUMBER: FHP-1-7190
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-692-9100; 1-206-224-0700 (direct)
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: page 4, RAR-alpha403 dominant negative; deleted of 1311-1596 of SEQ.
IMMEDIATE SOURCE:
LIBRARY: cDNA
US-08-592-483-3

Query Match 5.98; Score 74.4; DB 2; Length 2658;
Best local Similarity 60.38; Pred. No. 2 9e-10;
Matches 123; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 286 TGGCGCTGTGTAGCGATTACGATGATATGAGAGTGGTGGTGGTGAAGGA 345
DB 364 TCGTTGTCTGTGAGGACAGAGTGTGAGGCTACGCTAGGCTGTGAGAGG 423
QY 446 TGTAAAGCCGTTTAAAGAACATTCAGGACATATGATATTTGTCACCTACA 405
DB 424 TCGAAGCGCTTCTCGCCGACATCCAGGAAGACATGCTGACGCTGACACGAGC 483
QY 406 AATCAGCTGATCATATCAATAAAGACGAGGACAGAGTGTGAGGCTGTGAGGAG 465
DB 484 AAGAACTGCATCATCAACACAAAGGTGAGCGAAGATGCTGCTGCTGCTGCTGCTG 543
QY 466 TGTACGAAGTGGGAATGTGTGAAG 489
DB 544 TCGTTGAAGTGGGACATGTCCAG 567

RESULT 32
US-08-095-728B-3
Sequence 3, Application US/08095728B
Patent No. 5843642
GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P

APPLICANT: MILLER JR, WILSON H
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 AVENUE OF THE AMERICANS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcrtlin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P.
REGISTRATION NUMBER: 28,678
REFERENCE/BOOKET NUMBER: 38694-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: hMAR ALPHA
FEATURE:
NAME/KEY: CDS
LOCATION: 103..1488
OTHER INFORMATION:
US-08-095-728B-3

Query Match 5.98; Score 74.4; DB 2; Length 2928;
Best local Similarity 60.38; Pred. No. 3e-10;
Matches 123; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 286 TGGCGCTGTGTAGCGATTACGATGATATGAGAGTGGTGGTGGTGAAGGA 345
DB 364 TCGTTGTCTGTGAGGACAGAGTGTGAGGCTACGCTAGGCTGTGAGAGG 423
QY 446 TGTAAAGCCGTTTAAAGAACATTCAGGACATATGATATTTGTCACCTACA 405
DB 424 TCGAAGCGCTTCTCGCCGACATCCAGGAAGACATGCTGACGCTGACACGAGC 483
QY 406 AATCAGCTGATCATATCAATAAAGACGAGGACAGAGTGTGAGGCTGTGAGGAG 465
DB 484 AAGAACTGCATCATCAACACAAAGGTGAGCGAAGATGCTGCTGCTGCTGCTGCTG 543
QY 466 TGTACGAAGTGGGAATGTGTGAAG 489
DB 544 TCGTTGAAGTGGGACATGTCCAG 567

RESULT 33
PCT-0992-03320A-3
Sequence 3, Application PCT/US9202320A
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER


```

; FILING DATE: 30-NOV-1988
; APPLICATION NUMBER: 129,331
; FILING DATE: 02-DEC-1987
; SEQ ID NO:1
; LENGTH: 2940
5171671-1

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Query Match 5.98; Score 74.4; DB 6; Length 2940;
Best Local Similarity 60.38; Seed No. 30710.

Matches 123; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Dy 286 TGGCTGTGTCACCGATTATCCCATGGAGTATCACTATGCACGCTTGCTGGTTGAAGA 345
||| ||||| || | | | | | | | | | | | |
Db 364 TGCTTTACTGTCAACGAACTCTAAGCCTACCACTATGGAGTCAAGGCTGTGTGAAGG 423

364 TGGTTTCTCTAGGACAAAGTCTCAAGCTAACCTATGGAGTCAAGTCTGAGGAG 423

424 TGCACGCGCTTTCTGCTGACGATGTA:AA:AA:ATGCTGAC:AG:AG:GAC 483

406 AATCAGTGTAC AATCGATTA AAAACCGGAGGAGCTGGAGCTGGAG 465
 484 AAGAACTGGATATTAATTAAGGTTGATCTTAAACCTGTTGAGTACCTGACAGAG 543

QY	466	TTTACGAACTCTGCAATGGTGAAG	489
DB	544	TGCTTTGAAGTGGGCATGTGCAAG	567

RESULT 36
US-08-306-691B-52

Patent No. 5734039

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

:		TITLE OF INVENTION:	ANTISENSE
:		TITLE OF INVENTION:	OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
:		NUMBER OF SEQUENCES:	55

CONTACT OFFICE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia

```

: STATE: PENNSYLVANIA
:
: COUNTRY: U.S.A.
:
: ZIP: 19102
:
: COMPUTER READABLE FORM:

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COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: HHS/08/306,641R
 FILING DATE: September 15, 1994
 CLASSIFICATION: 514

: PRIOR APPLICATION (AIA):
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 :

NAME: MONACO, DANIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 508-6103
TELEFAX: (215) 508-5549
FLEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 52:

```

; SEQUENCE CHARACTERISTICS:
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; LENGTH: 3036 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;

```

US-08-306-691B-52

Query Match	5.98;	Score 74.4;	DB 1;	Length 3036;
Best Local Similarity	60.38,	Pred. No. 3.1e+10,		
Matches 123;	Conservative 0;	Mismatches 81;	Indels 0;	Gaps 0;

286 TCGCGTGTCTTCGACACCGATTACCGCATTCGCGATATCAGCTATTCGACTCTCTGCTGCTTCCTCAACCGA 345

346 TTTAAAGCTTTTAAAAAGAAATTTAAGGATATATGATTATATTGTCCAGCTACA 405

D0 193 TGTAAAGGCTTCTTCCTGGACAGATCTCAGAASAAATATTTCTTAACCGTGCAATCCGAAT 1452

DY 406 AATTATGATGATAAATGATAAAAAAGTGGTAAAGTATGATTAATGATGATGATGATGATGATGATGAT 465

1453 AAGACGATCATCAACAAAGTGGACCTGGAACTGCTGCTAGCTGGTACCTGACGAG 1512

Db 1513 TCGTTGAAGTGGGATGTCCAG 1536

RESOLUT 37
US-08-095-728B-1
Statement 1, Application US 608095728B
Patent No. 5843642

GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: MILLER JR, WILSON H

APPLICANT: FRANKEL, STANLEY	
TITLE OF INVENTION: METHODS FOR THE DETECTION AND	
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)	
NUMBER OF SEQUENCES: 11	

:
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: COOPER & DUNHAM LLP
 :
 : STREET: 1185 AVENUE OF THE AMERICAS
 :
 : CITY: NEW YORK
 :

```

: STATE: NEW YORK
: COUNTRY: U S A
: ZIP: 10036
: COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; COMMENT: Data file, Release #1.34

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 05/08/095 728B
3 FILING DATE: 21-JUL-1993
4 INVENTOR: ADK

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ABSTRACT/CLAIMS INTRODUCTION

NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-A
REGISTRATION STATE: MISSOURI

TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO. 1

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; LENGTH: 3036 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MONOMER: 1

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; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONF: MYL-PAR
;
PROTEIN
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```

; NAME/KEY: CDS
; LOCATION: 67.2457
; OTHER INFORMATION:

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FEATURE:
NAME/KEY: misc_feature
LOCATION: 303..304
OTHER INFORMATION: /note: "Gap in DNA sequence of
OTHER INFORMATION: undetermined length"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1197..1198
OTHER INFORMATION: /note: "Gap in DNA sequence of
OTHER INFORMATION: undetermined length"
FEATURE:
NAME/KEY: exon
LOCATION: 534..600
US-08-312-412A-1

Query Match      5 98: Score 74.4  DR 1: Length 3466
Best Local Similarity 81.78: Pred. No. 3,2e-10:
Matches 98: Conservative 0: Mismatches 21: Indels 1: Gaps 1:

QY 475 AGGATATATGATATTTGTGAGCTACCAATCAGTGTAAATGATATGAAAAAGCCGAG 434
DB 602 AATGATATATGATATGATGTTGATGATGATGATGATGATGATGATGATGATGAT 542
QY 435 CAAGAGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
DB 542 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434

RESULT 40
US-08-892-747-13
Sequence 14, Application US/08892747
Patent No. 6057153
GENERAL INFORMATION:
APPLICANT: Shaji T. George, Michael M. Martina Werner,
APPLICANT: Umberto Pace and Allan R. Goldberg
TITLE OF INVENTION: Stabilized External Guide Sequences
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,747
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/472,556
FILING DATE: January 13, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00514
FILING DATE: January 19, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 111109C192
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3511 base pairs
TYPE: nucleic acid

```

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..3511
OTHER INFORMATION: /function: "PMU-RAR DNA Sequence."
US-08-892-747-13

Query Match      5 98: Score 74.4  DR 3: Length 3511:
Best Local Similarity 60.38: Pred. No. 3,2e-10:
Matches 123: Conservative 0: Mismatches 81: Indels 0: Gaps 0:

QY 386 TCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 345
DB 1898 TCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1867
QY 346 TGTAAAGCCCTTTTAAAGAGCATTCAGGACATATGATTATTTGTCAGCTACA 405
DB 1868 TGTAAAGCCCTTTTAAAGAGCATTCAGGACATATGATTATTTGTCAGCTACA 1427
QY 406 AATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 405
DB 1928 AATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1987
QY 466 TGTAAAGCTGCGAATGCTGAG 489
DB 1988 TGTAAAGCTGCGAATGCTGAG 2011

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Search completed: June 16, 2003, 04:20:50
 Job time : 62.1909 secs



94 64.8 5.2 1404 10 US 09 965-703 62 Sequence 62, Appl
94 64.8 5.2 2711 13 US 09 952-559 2 Sequence 63, Appl
95 64.4 5.1 4811 10 US 09 864-761 16445 Sequence 16445, A
96 64 5.1 440 9 US 09-918-995-42194 Sequence 42194, A
97 64.2 4.9 5449 9 US 09-991-946-1417 Sequence 1417, Ap
98 6.2 4.9 1759 10 US 09-962-446-300 Sequence 300, App
99 6.2 4.9 5642 12 US 10 002-600 54 Sequence 54, Appl
100 60.8 4.8 198 10 US 09-965-703 41 Sequence 41, Appl
101 60.8 4.8 1247 10 US 09-965-703 41 Sequence 41, Appl
102 60.8 4.8 1288 10 US 09-965-703 41 Sequence 70, Appl
103 60.8 4.8 1290 10 US 09-965-697 4 Sequence 1, Appl
104 60.8 4.8 1542 10 US 09-965-703 58 Sequence 58, Appl
105 60.8 4.8 2065 12 US 10 142-373 1 Sequence 1, Appl
106 60.4 4.8 987 10 US 09-965-703 21 Sequence 21, Appl
107 60.4 4.8 1398 10 US 09-909-672 1 Sequence 1, Appl
108 60.2 4.8 2511 10 US 09 919 497 46 Sequence 46, Appl
109 60 4.8 392 9 US 10-052-092 4 Sequence 4, Appl
110 60 4.8 1237 9 US 10-052-092 3 Sequence 3, Appl
111 58.8 4.7 643 9 US 09-918-995-15693 Sequence 15693, A
112 58.8 4.7 1740 9 US 10 161-803 26 Sequence 26, Appl
113 57 4.5 2751 10 US 09-728 422 2 Sequence 2, Appl
114 56 4.5 486 9 US 09-918 995 13740 Sequence 13740, A
115 56 4.5 1123 10 US 09-965-703 26 Sequence 26, Appl
116 55.8 4.4 2066 10 US 09 895-840 1 Sequence 1, Appl
117 55.8 4.4 2126 9 US 10 295 470 1 Sequence 470, App
118 55.2 4.4 571 9 US 10 066 543 458 Sequence 4, Appl
119 55.2 4.4 1837 9 US 10 295 470 3 Sequence 1, Appl
120 54.6 4.3 1383 10 US 09 731 557A 1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US 10 198 785 1 Application US/10198785
? Sequence 1, Application US/10198785
? Publication No. US200 0022224A1
? GENERAL INFORMATION
? APPLICANT: CITIMUS OPTICAL CO., LTD.
? TITLE OF INVENTION: Method of detecting binding reaction between protein and test sub
? FILE REFERENCE: 781-0280548
? CURRENT APPLICATION NUMBER: US/10/198 785
? CURRENT FILING DATE: 2002 07 19
? PRIOR APPLICATION NUMBER: JP/2001 220444
? PRIOR FILING DATE: 2001 07 19
? PRIOR APPLICATION NUMBER: JP/2001 221963
? PRIOR FILING DATE: 2001 07 23
? NUMBER OF SEQ ID NOS: 3
? SOFTWARE: PatoutIn Ver. 2.0
? SEQ ID NO: 1
? LENGTH: 1740
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (99) .. (1688)
US 10 198 785 1

Query Match 99.28: Score 1247: DB 9: Length 1740:

Best Local Similarity 100.0%: Prod. No. 0:
Matches 1247: Conserved 0: Mismatches 0: Indels 0: Gaps 0:

UY 1 ATGATTAATACATCTGACAAATGCTAACTTGTGAAGAGTGGCTGGTGGAGAGC 60
DB 1 ATGATTAATACATCTGACAAATGCTAACTTGTGAAGAGTGGCTGGTGGAGAGC 60
UY 258 ATGATTAATACATCTGACAAATGCTAACTTGTGAAGAGTGGCTGGTGGAGAGC 417
DB 258 ATGATTAATACATCTGACAAATGCTAACTTGTGAAGAGTGGCTGGTGGAGAGC 417
UY 61 ACAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 120
DB 61 ACAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 120
UY 418 ACAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 477
DB 418 ACAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 477
UY 121 CACTTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 180
DB 121 CACTTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 180
UY 478 CACTTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 437
DB 478 CACTTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 437

UY 181 GAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 240
DB 181 GAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 240
UY 438 GAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 497
DB 438 GAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 497
UY 241 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 300
DB 241 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 300
UY 438 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 557
DB 438 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 557
UY 401 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 460
DB 401 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 460
UY 558 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 617
DB 558 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 617
UY 361 AAAAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 420
DB 361 AAAAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 420
UY 618 AAAAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 677
DB 618 AAAAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 677
UY 441 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 540
DB 441 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 540
UY 738 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 797
DB 738 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 797
UY 541 AGTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 600
DB 541 AGTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 600
UY 738 AGTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 857
DB 738 AGTATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 857
UY 601 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 660
DB 601 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 660
UY 858 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 917
DB 858 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 917
UY 661 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 720
DB 661 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 720
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DB 918 GCAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 977
UY 721 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 780
DB 721 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 780
UY 978 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1037
DB 978 ATGATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1037
UY 781 AAAAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 840
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DB 1038 AAAAAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1097
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DB 841 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 900
UY 1098 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1157
DB 1098 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1157
UY 901 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 960
DB 901 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 960
UY 1158 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1217
DB 1158 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1217
UY 961 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1020
DB 961 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1020
UY 1218 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1277
DB 1218 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1277
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UY 1081 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1140
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UY 1141 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1200
DB 1141 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1200
UY 1398 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1457
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UY 1201 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1247
DB 1201 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1247
UY 1458 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1504
DB 1458 GATTAATCAATATGTTGTTGTTCAAAATCTGGAGACCTTGTGCTTACCTGCTCAATG 1504

QY 1043 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1042
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1481 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1540
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 QY 1102 -GACAGACGCGGAGAACTGGCTGCTCTGTCACCGCTGAGCCGATGCTTTCGTTTGGG 1159
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 Db 1601 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1660
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 QY 1160 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1219
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 Db 1661 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1720
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 QY 1220 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1247
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 Db 1721 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1748
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RESULT 24

US-09-853-033-7
 : Sequence 7, Application US/09853033
 : Patent No. US2002010068A1
 : GENERAL INFORMATION:
 : APPLICANT: CHAMBER, PIERRE
 : APPLICANT: MEIZGER, DANIEL
 : TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
 : FILE REFERENCE: 065691/0232
 : CURRENT APPLICATION NUMBER: US/09/853,033
 : PRIORITY FILING DATE: 2001-05-11
 : PRIORITY FILING DATE: 2000-10-04
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: Patent In Ver. 2.1
 : SEQ ID NO 7
 : LENGTH: 1983
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (1)..(1983)
 : OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence
 : OTHER INFORMATION: Homosapiens-Bacteriophage p1
 US-09-853-033-7

Query Match: 17.48; Score 218.4; DB 10; Length 1983;
 Host Local Similarity 61.54; Pred No 46-57;
 Matches 386; Conservative 0; Mismatches 236; Indels 6; Gaps 2;

QY 626 GCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 685
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1121 GCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1180
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 686 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 742
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1181 GCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1240
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 743 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 802
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1241 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1300
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 QY 803 AGGCGATGATCTGCTCAATTCGAGTATGAGTCTCTGTCATATGAGAGTCAAGCAATCT- 862
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 Db 1301 AGGCGATGATCTGCTCAATTCGAGTATGAGTCTCTGTCATATGAGAGTCAAGCAATCT- 1360
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 863 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 922
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1361 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1420
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 923 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 982
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

Db 1421 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1480
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 983 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1042
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1481 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1540
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 1043 AGGCGATGATCTGCTCAATTCGAGTATGAGTCTCTGTCATATGAGAGTCAAGCAATCT- 1101
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1541 AATCTATATTTTGTCTTAATTTCTGAGTGTATACATTTCTGTCTGAGTACCTTGAATCTTC 1600
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 1102 -GACAGACGCGGAGAACTGGCTGCTCTGTCACCGCTGAGCCGATGCTTTCGTTTGGG 1159
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1601 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1660
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 1160 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1219
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1661 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1720
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 1220 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1247
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 1721 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 1748
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

RESULT 24

US-10-052-092-2
 : Sequence 2, Application US/10052092
 : Publication No. US2003002778A1
 : GENERAL INFORMATION:
 : APPLICANT: Fuqua, Suzanne
 : APPLICANT: Alfred, D.
 : APPLICANT: Haff, Torsten A.
 : APPLICANT: O'Connell, Peter
 : TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapy
 : FILE REFERENCE: P02102952
 : CURRENT APPLICATION NUMBER: US/10/052,092
 : CURRENT FILING DATE: 2002-01-18
 : PRIORITY FILING DATE: US 60/262,990
 : PRIORITY FILING DATE: 2001-01-19
 : PRIORITY APPLICATION NUMBER: US 60/104,018
 : PRIORITY FILING DATE: 2001-07-09
 : NUMBER OF SEQ ID NOS: 49
 : SOFTWARE: Patent In version 3.1
 : SEQ ID NO 2
 : LENGTH: 1644
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Synthetic Estrogen Receptor Ligand Binding Domain Fusion
 : OTHER INFORMATION: Synthetic Estrogen Receptor Ligand Binding Domain Fusion
 US-10-052-092-2

Query Match: 17.48; Score 216.8; DB 9; Length 1644;
 Host Local Similarity 61.54; Pred No 8.46-57;
 Matches 385; Conservative 0; Mismatches 237; Indels 6; Gaps 2;

QY 626 GCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 685
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 782 GCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 841
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 686 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 742
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 842 GCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 901
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 743 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 802
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 902 TCGGACGCGGACGAGTATGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 961
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 803 AGGCGATGATCTGCTCAATTCGAGTATGAGTCTCTGTCATATGAGAGTCAAGCAATCT- 862
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 Db 962 AGGCGATGATCTGCTCAATTCGAGTATGAGTCTCTGTCATATGAGAGTCAAGCAATCT- 1021
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 QY 863 TGGTAATACCTTCAGAGTTTGGAGTTAAATTCGACACAAAGCAATATCTCTGTGCA 922
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 41
 LENGTH: 2775
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Synthesized
 US 09-908 1548 41

Query Match 16.0% Score 200.8; ID# 9; Length 2775;
 Best Local Similarity 61.7% Pred. No. 1 to 51;
 Matches 348; Conservative 0; Mismatches 207; Indels 4; Gaps 1;

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UY 703 CCTTTCAGAGAGGCTGACATGATGATGCTGCAAGCTTGCGGACAGAGAGTGGTGA 762
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 748 CCTTTCAGAGAGGCTGACATGATGATGCTGCAAGCTTGCGGACAGAGAGTGGTGA 807
UY 763 CATATCATTAACCTGAGGAAAGAGATTCCTGCTGGTGTGAGTTCAGCTTCAGTAA 822
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 808 CATATCATTAACCTGAGGAAAGAGATTCCTGCTGGTGTGAGTTCAGCTTCAGTAA 867
UY 823 GTGCGGCTCTTTCAGAGAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 882
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 868 GTGCGGCTCTTTCAGAGAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 927
UY 883 ATTGACATCCGCGGAGAGCTGATCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTG 942
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 928 ATTGACATCCGCGGAGAGCTGATCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTG 987
UY 943 AAATGCTGACAGAGAGATTCGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCT 1002
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 988 AAATGCTGACAGAGAGATTCGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCT 1047
UY 1003 GAGAGCTTAAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1062
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1048 GAGAGCTTAAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1107
UY 1063 TCTAGATGATGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1122
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1108 TCTAGATGATGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1167
UY 1123 GAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1179
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1158 GAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1227
UY 1180 TCTTTCAGAGAGATTCAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAG 1249
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1228 ACTGTCAGAGAGATTCAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAG 1287
UY 1240 CATGCTGAG 1247
    |||||
DB 1288 CATATCAG 1295

```

RESULT 43
 US 09-908 1548 41/25

Sequence 43: Application US/09-081548
 Patent No. US20020168714A1
 GENERAL INFORMATION:
 APPLICANT: Hutch, Carlos F.
 APPLICANT: Hutch, Roger
 APPLICANT: Schopfer, Ulrich
 TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
 TITLE OF INVENTION: SINGLE CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
 FILE REFERENCE: TSK1 725.1
 CURRENT APPLICATION NUMBER: US/09/908, 1548
 PRIOR FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: US 69/619,063
 PRIOR FILING DATE: 2000-07-18
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 43
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Synthesized
 US 09-908 1548-43

Query Match 16.0% Score 200.8; ID# 9; Length 2775;
 Best Local Similarity 61.7% Pred. No. 1 to 51;
 Matches 348; Conservative 0; Mismatches 207; Indels 4; Gaps 1;

```

UY 703 CCTTTCAGAGAGGCTGACATGATGATGCTGCAAGCTTGCGGACAGAGAGTGGTGA 762
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2028 CCTTTCAGAGAGGCTGACATGATGATGCTGCAAGCTTGCGGACAGAGAGTGGTGA 1969
UY 763 CATATCATTAACCTGAGGAAAGAGATTCCTGCTGGTGTGAGTTCAGCTTCAGTAA 822
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1968 CATATCATTAACCTGAGGAAAGAGATTCCTGCTGGTGTGAGTTCAGCTTCAGTAA 1909
UY 823 GTGCGGCTCTTTCAGAGAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 882
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1908 GTGCGGCTCTTTCAGAGAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1849
UY 883 ATTGACATCCGCGGAGAGCTGATCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTG 942
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1848 ATTGACATCCGCGGAGAGCTGATCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTG 1789
UY 943 AAATGCTGACAGAGAGATTCGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCT 1002
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1788 AAATGCTGACAGAGAGATTCGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCT 1729
UY 1003 GAGAGCTTAAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1062
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1728 GAGAGCTTAAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1669
UY 1063 TCTAGATGATGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1122
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1668 TCTAGATGATGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1609
UY 1123 GAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1179
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1608 GAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCA 1549
UY 1180 TCTTTCAGAGAGATTCAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAG 1249
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1548 ACTGTCAGAGAGATTCAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAGCTTCTGCAAG 1489
UY 1240 CATGCTGAG 1247
    |||||
DB 1488 CATATCAG 1481

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RESULT 44
 US 09-962-436-268

Sequence 268: Application US/09962436
 Patent No. US20020081801A1
 GENERAL INFORMATION:
 APPLICANT: Soppet, Daniel
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Stem
 TITLE OF INVENTION: SCS
 FILE REFERENCE: 689290-75
 CURRENT APPLICATION NUMBER: US/09/962,436
 PRIOR APPLICATION NUMBER: US/60/245,082
 PRIOR FILING DATE: 2000-09-25
 PRIOR APPLICATION NUMBER: US/60/244,924
 PRIOR FILING DATE: 2000-09-25
 NUMBER OF SEQ ID NOS: 508
 SOFTWARE: Patent to version 4.0
 SEQ ID NO 268
 LENGTH: 2218
 TYPE: DNA

ORGANISM: Homo sapiens
US-08-826-361a-20

Query Match 10.4% Score 143 P. DB 10 Length 2402
Best Local Similarity 49.98% Pred. No. 71e-31;
Matches 392; Conservative 0; Mismatches 347; Indels 6; Gaps 2;

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QY 280 CACTTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 340 GAAGCATGTAAGGCTTTTAAAGAACATTCAGGACATTAATGATATATGTGCA 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 GAGGCTGTGAAAGGCTTTTAAAGAACATTCAGGACATTAATGATATATGTGCA 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 GTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 460 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 ACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 520 CCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 646 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 580 ATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 706 CCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 766 GCTGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 825
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 700 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 826 CCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 760 GTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 883 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 820 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 943 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 880 TCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1003 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 940 GTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1063 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 1122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1000 TTTGCAATGATTAATATGATGATGATGATGATGATGATGATGATGATGAT 1059
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1120 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 1179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1060 AATTG 1064
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1180 AATTG 1184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 35

US-10-211-239-7
Sequence 7: Application US/10211249
Publication No. US20040103965A1
GENERAL INFORMATION:
APPLICANT: Jung, Hyeon
APPLICANT: Kraft, No. US20040103965A1
APPLICANT: Mueller, Stefan
TITLE OF INVENTION: Method for Identifying Substances Which Positively

TITLE OF INVENTION: Influence Inflammatory Conditions
FILE REFERENCE: 0652,2340001
CURRENT APPLICATION NUMBER: US/10/211,239
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 60/315,775
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: EP 0119003.0
PRIOR FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 2402
TYPE: DNA
ORGANISM: Homo sapiens
US-10-211-239-7

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QY 280 CACTTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 583 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 340 GAAGCATGTAAGGCTTTTAAAGAACATTCAGGACATTAATGATATATGTGCA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 643 GAGGCTGTGAAAGGCTTTTAAAGAACATTCAGGACATTAATGATATATGTGCA 702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 GTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 703 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 460 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 763 ACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 520 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 823 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 580 ATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 883 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 820 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 943 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 880 TCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1003 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 940 GTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1063 GCGCTGTGGCTGTGCAATGATTACGATGGGAAATATCATATGATGCTGCTGT 1122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1000 TTTGCAATGATTAATATGATGATGATGATGATGATGATGATGATGATGAT 1059
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1120 CCAATATGTTAGCAAGTGGGAATGCTGAAGTGTGCTGCTGCAAGATATGCTGA 1179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1060 AATTG 1064
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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1826 AAGCAGGATACCTCTTAAATCTTAAATTAATCAATCAATCTGGAAATCTAAAATCTTAAG 1885
 531 GATATATCAATCTGCGACGACGATCTCTGCTGGCGCAAGGCTAAATATATCTGGCG 590
 1886 AATAAATGAATCTTCTAATCTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1945
 591 CCACT 650
 1946 TCTCAATATTGAAGCTATGAGT-----TGAAGCAATCTTCTTAATCTTC 1992
 651 CACT 710
 1993 CTGGAAGCATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2051
 711 CGAGCT 770
 2052 CTTTCAATCTTCT 2111
 771 CAGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 830
 2112 CAGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2171
 831 CTTGATAGCTCTTCTGATAGCTCTTCTGATAGCTCTTCTGATAGCTCTTCTGATAGCTCTTCT 884
 2172 CATCTATCT 2231
 885 TCACTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 926
 2232 TCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2273

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RESEQ ID: 38
US-09-997-267-1
Sequence 1: Application US/09997267
Patent No: US2002015581A1
GENERAL INFORMATION:
APPLICANT: AHRENS-PATH, ISABELLE
APPLICANT: HAENDLER, BERNARD
TITLE OF INVENTION: HUMAN AND/OR FN PROTEIN VARIANTS
FILE REFERENCE: SCH-1793
CURRENT APPLICATION NUMBER: US/09/997 267
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/255,978
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 1
LENGTH: 1329
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-267-1

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	Query Match	7.63	Score 95.75	Pr 9.10	Length 1499
	Best Local Similarity	51.28		Prod. No. 5.76-19	
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QY	285	CTGGCGTCTGCTGACGATTTGCTATGATGATATGATGATGCTGCTGCTGCTGATGAG	344		
DB	243	CTGGCTGATCTGTGATGATTAAGCTTTGGCTGTGCTATGATGAGCTCTATATGATGAG	302		
QY	345	ATGTGAGGCTTTTAAAGACAGCATTCAGGACATATGATTAATTTGCTAACTAC	404		
DB	303	CTGGTAAGCTCTCTTCTGAAAAGAGCTCTGTAAGGAAAACAAGATCTCTGTGATGATGAG	362		
QY	405	AAATATGCTATATGCTATAAAGAGCTGGAGTAAAGCTGGACGCTGGAGTATGGAAA	464		
DB	363	AAATATATCTACTATTTGCTAAATTCGCAAGGAAAAAATTTGCATCTTTCTGGCTTGGAAA	422		
QY	465	GTCTTATCAACCTGGCAATCTGTAATTTCTGCTGGAGAGAGATGCTGATGCTGCT	524		
DB	423	ATCTATATGACGATGATGATGCTGTGGAGAGCTGTAAGCTGTAAGCTTATATGTTGAA	482		

[illegible]

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1  RESULT 19
2  US-09-880-107-2300
3  ? Sequence 2300, Application US/09880107
4  ? Patent No. US20020142981A1
5  ? GENERAL INFORMATION:
6  ? APPLICANT: Horne, Darci L.
7  ? APPLICANT: Wockley, Joseph G.
8  ? APPLICANT: Scherff, Jue
9  ? APPLICANT: Gene Logic, Inc.
10 ? TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
11 ? FILE REFERENCE: 44921-5028-WO
12 ? CURRENT APPLICATION NUMBER: US/09/880,107
13 ? CURRENT FILING DATE: 2001-06-14
14 ? PRIOR APPLICATION NUMBER: US 60/211,379
15 ? PRIOR FILING DATE: 2000-06-14
16 ? PRIOR APPLICATION NUMBER: US 60/247,054
17 ? PRIOR FILING DATE: 2000-10-02
18 ? NUMBER OF SEQ ID NOS: 3950
19 ? SOFTWARE: Patent In Ver. 2.1
20 ? SEQ ID NO 2300
21 ? LENGTH: 4715
22 ? TYPE: DNA
23 ? ORGANISM: Homo sapiens
24 ? FEATURE:
25 ? TYPE: INFORMATION, Genbank Accession No. US20020142981A1 M23263
26 ? US-09-880-107-2300

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[illegible]

